



amdt a

SEQUENCE LISTING

Sub
24

<110> Wright, David A.
Voytas, Daniel F.

<120> Plant Retroelements and Methods Related Thereto

<130> P-1065A

<140> 09/586,106
<141> 2000-06-02

<150> 60/087,125
<151> 1998-05-29

<150> 09/322,478
<151> 1999-05-28

<160> 169

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "plant
retroelement sequence"

<400> 4

Met Ala Ser Arg Lys Arg Lys

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<210> 5

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 5

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<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 6

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Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr
20 25 30

Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu

35					40					45					
Leu	Gly	Pro	Gly	Met	Phe	Asp	Glu	Phe	Leu	Gln	Glu	Leu	Gln	Arg	Leu
50					55					60					
Arg	Trp	Asp	Gln	Val	Leu	Thr	Arg	Leu	Pro	Glu	Lys	Trp	Ile	Asp	Val
65					70					75					80
Ala	Leu	Val	Lys	Glu	Phe	Tyr	Ser	Asn	Leu	Tyr	Asp	Pro	Glu	Asp	His
				85					90					95	
Ser	Pro	Lys	Phe	Trp	Ser	Val	Arg	Gly	Gln	Val	Val	Arg	Phe	Asp	Ala
			100					105					110		
Glu	Thr	Ile	Asn	Asp	Phe	Leu	Asp	Thr	Pro	Val	Ile	Leu	Ala	Glu	Gly
		115					120					125			
Glu	Asp	Tyr	Pro	Ala	Tyr	Ser	Gln	Tyr	Leu	Ser	Thr	Pro	Pro	Asp	His
	130					135					140				
Asp	Ala	Ile	Leu	Ser	Ala	Leu	Cys	Thr	Pro	Gly	Gly	Arg	Phe	Val	Leu
145					150					155					160
Asn	Val	Asp	Ser	Ala	Pro	Trp	Lys	Leu	Leu	Arg	Lys	Asp	Leu	Met	Thr
			165					170						175	
Leu	Ala	Gln	Thr	Trp	Ser	Val	Leu	Ser	Tyr	Phe	Asn	Leu	Ala	Leu	Thr
		180					185					190			
Phe	His	Thr	Ser	Asp	Ile	Asn	Val	Asp	Arg	Ala	Arg	Leu	Asn	Tyr	Gly
		195					200					205			
Leu	Val	Met	Lys	Met	Asp	Leu	Asp	Val	Gly	Ser	Leu	Ile	Ser	Leu	Gln
	210					215					220				
Ile	Ser	Gln	Ile	Ala	Gln	Ser	Ile	Thr	Ser	Arg	Leu	Gly	Phe	Pro	Ala
225					230					235					240
Leu	Ile	Thr	Thr	Leu	Cys	Glu	Ile	Gln	Gly	Val	Val	Ser	Asp	Thr	Leu
				245					250					255	
Ile	Phe	Glu	Ser	Leu	Ser	Pro	Val	Ile	Asn	Leu	Ala	Tyr	Ile	Lys	Lys
		260						265					270		
Asn	Cys	Trp	Asn	Pro	Ala	Asp	Pro	Ser	Ile	Thr	Phe	Gln	Gly	Thr	Arg
	275					280						285			
Arg	Thr	Arg	Thr	Arg	Ala	Ser	Ala	Ser	Ala	Ser	Glu	Ala	Pro	Leu	Pro
	290					295					300				
Ser	Gln	His	Pro	Ser	Gln	Pro	Phe	Ser	Gln	Arg	Pro	Arg	Pro	Pro	Leu
305					310					315					320
Leu	Ser	Thr	Ser	Ala	Pro	Pro	Tyr	Met	His	Gly	Gln	Met	Leu	Arg	Ser
				325					330					335	
Leu	Tyr	Gln	Gly	Gln	Gln	Ile	Ile	Ile	Gln	Asn	Leu	Tyr	Arg	Leu	Ser

340

345

350

Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg
 355 360 365

Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu
 370 375 380

Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp
 385 390 395 400

Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu
 405 410 415

Gly Arg Gly Ser Glx
 420

<210> 7

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 7

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 acctcacctc ctcttctctc aaattatgct cagatggacg gggaaccggc acaaagagtc 180
 acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg 240
 gaagtccaag cagatctcct tactcaaggg aacctcttcc atggtcttcc aaatgaagat 300
 ccatatgcgc atctagcctc atacatagag atatgcagca ccgttaaaat cgccggagtt 360
 ccaaaagatg cgatactcct taacctcttt tcttttccc tagcaggaga ggcaaaaaga 420
 tggttgcact cctttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc 480
 ttaaagaagt atttccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatttc 540
 catcaatttc tggatgaatc ccttagcgaa gcactagacc atttccacgg attgctaaga 600
 aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg 660
 caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720
 atggagctcg tcgagaacat ggcggttagc gatcaagcaa tccttcatga tcacacttat 780
 gttccacaaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac 840
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<210> 8
 <211> 532
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 8

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Ile	Glu	Ala	Thr	Cys	Arg	Arg	Asn	Asn	Ala	Ala	Arg	Arg	Arg	Arg	Glu	20	25	30	
Gln	Asp	Ile	Glu	Gly	Ser	Ser	Tyr	Thr	Ser	Pro	Pro	Pro	Ser	Pro	Asn	35	40	45	
Tyr	Ala	Gln	Met	Asp	Gly	Glu	Pro	Ala	Gln	Arg	Val	Thr	Leu	Glu	Asp	50	55	60	
Phe	Ser	Asn	Thr	Thr	Thr	Pro	Gln	Phe	Phe	Thr	Ser	Ile	Thr	Arg	Pro	65	70	75	80
Glu	Val	Gln	Ala	Asp	Leu	Leu	Thr	Gln	Gly	Asn	Leu	Phe	His	Gly	Leu	85	90	95	
Pro	Asn	Glu	Asp	Pro	Tyr	Ala	His	Leu	Ala	Ser	Tyr	Ile	Glu	Ile	Cys	100	105	110	
Ser	Thr	Val	Lys	Ile	Ala	Gly	Val	Pro	Lys	Asp	Ala	Ile	Leu	Leu	Asn	115	120	125	
Leu	Phe	Ser	Phe	Ser	Leu	Ala	Gly	Glu	Ala	Lys	Arg	Trp	Leu	His	Ser	130	135	140	
Phe	Lys	Gly	Asn	Ser	Leu	Arg	Thr	Trp	Glu	Glu	Val	Val	Glu	Lys	Phe	145	150	155	160
Leu	Lys	Lys	Tyr	Phe	Pro	Glu	Ser	Lys	Thr	Val	Glu	Arg	Lys	Met	Glu	165	170	175	
Ile	Ser	Tyr	Phe	His	Gln	Phe	Leu	Asp	Glu	Ser	Leu	Ser	Glu	Ala	Leu	180	185	190	
Asp	His	Phe	His	Gly	Leu	Leu	Arg	Lys	Thr	Pro	Thr	His	Arg	Tyr	Ser	195	200	205	
Glu	Pro	Val	Gln	Leu	Asn	Ile	Phe	Ile	Asp	Asp	Leu	Gln	Leu	Leu	Ile	210	215	220	
Glu	Thr	Ala	Thr	Arg	Gly	Lys	Ile	Lys	Leu	Lys	Thr	Pro	Glu	Glu	Ala	225	230	235	240
Met	Glu	Leu	Val	Glu	Asn	Met	Ala	Ala	Ser	Asp	Gln	Ala	Ile	Leu	His	245	250	255	

Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr
 260 265 270
 Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu
 275 280 285
 Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile
 290 295 300
 Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys
 305 310 315 320
 Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser
 325 330 335
 Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly
 340 345 350
 Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe
 355 360 365
 Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly
 370 375 380
 Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln
 385 390 395 400
 Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln
 405 410 415
 Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys
 420 425 430
 Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu
 435 440 445
 Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr
 450 455 460
 Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys
 465 470 475 480
 Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val
 485 490 495
 Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu
 500 505 510
 Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala
 515 520 525
 Arg Glu Ala Lys
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<210> 9

<211> 603
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

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 tcccgttttg gagtccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat 300
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 cctcagacaa atggccaagc agaaatttct aacagggagc tcaagcgaat cctggaaaag 420
 acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat 480
 aggacagcgt tcaagactcc catcggttta tcaccatttc agctagtgtg tgggaaggca 540
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 gac 603

<210> 10
 <211> 201
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 10
 Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met
 1 5 10 15
 Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile
 20 25 30
 Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu
 35 40 45
 Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro
 50 55 60
 Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe
 65 70 75 80
 Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His
 85 90 95
 Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg
 100 105 110
 His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu
 115 120 125
 Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser

130 135 140

Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr
 145 150 155 160

Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val
 165 170 175

Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr
 180 185 190

Trp Ala Leu Lys Leu Leu Asn Phe Asp
 195 200

<210> 11
 <211> 600
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 11
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 gttcccaaga aagggtggaat gacagtggta cgagatgaga ggaatgactt gataccaaca 120
 cgaactgtca ctggttggcg aatgtgtatc gactatcgca agctgaatga agccacacgg 180
 aaggaccatt tccccttacc tttcatggat cagatgctgg agagacttgc agggcaggca 240
 tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga cccagagat 300
 caggagaaga cggcctttac atgccccttt ggcgtctttg cttacagaag gatgccattc 360
 gggttatgta atgcaccagc cacatttcag aggtgcatgc tggccatttt ttcagacatg 420
 gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatgtgac 480
 agctgtttga ggaacctaga gagggactt cagaggtgcg aagagactaa cttggtactg 540
 aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca 600

<210> 12
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 12
 Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser Ala Trp Val Ser
 1 5 10 15

Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr Val Val Arg Asp
 20 25 30

Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr Gly Trp Arg Met
 35 40 45

Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp His Phe

50					55					60					
Pro	Leu	Pro	Phe	Met	Asp	Gln	Met	Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala
65					70					75					80
Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val
				85					90					95	
Asp	Pro	Arg	Asp	Gln	Glu	Lys	Thr	Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val
			100					105					110		
Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr
		115					120					125			
Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile	Phe	Ser	Asp	Met	Val	Glu	Lys	Ser
		130					135					140			
Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val	Phe	Gly	Pro	Ser	Phe	Asp
145					150					155					160
Ser	Cys	Leu	Arg	Asn	Leu	Glu	Arg	Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr
				165					170					175	
Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Arg	Glu	Gly
			180					185					190		
Ile	Val	Leu	Gly	His	Lys	Ile	Ser								
		195					200								

<210> 13

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
retroelement sequence

<400> 13

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aacaaggagc	gttactttgc	acgtttcttg	gaaatattca	aaggggttaga	aatcactatg	120
ccattcgggg	aagccttaca	gcagatgccc	ctctactcca	aatttatgaa	agacatcctc	180
accaagaagg	ggaagtatat	tgacaacgag	aatattgttg	taggaggcaa	ttgcagtgcg	240
ataatacaaa	ggattctacc	caagaagttt	aaagaccccg	gaagtgttac	catcccgtgc	300
accattggga	aggaagccgt	aaacaaggcc	ctcattgatc	taggagcaag	tatcaatctg	360
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cttcaactgg	cagaccgctc	aatcacaagg	ccatatgggg	tggtagaaga	tgtcctggtc	480
aaggtagccc	acttcacttt	tccggtggac	tttgttatca	tggatatcga	agaagacact	540
gagattcccc	ttatcttagg	cagacccttc	atgctgactg	ccaactgtgt	ggtggatatg	600
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gatgtcagtt	ttctcgagac	accaaagact	tcgctagaaa	aagcaatggt	aatcatttta	780
gactgtctaa	ccagtgaaga	ggaagaagat	ctgaaggctt	gcttggaana	cttgatcaa	840
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<210> 14
 <211> 286
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 14

Lys	Glu	Glu	Pro	Leu	Ala	Leu	Pro	Gln	Asp	Leu	Pro	Tyr	Pro	Met	Ala	1	5	10	15
Pro	Thr	Lys	Lys	Asn	Lys	Glu	Arg	Tyr	Phe	Ala	Arg	Phe	Leu	Glu	Ile	20	25	30	
Phe	Lys	Gly	Leu	Glu	Ile	Thr	Met	Pro	Phe	Gly	Glu	Ala	Leu	Gln	Gln	35	40	45	
Met	Pro	Leu	Tyr	Ser	Lys	Phe	Met	Lys	Asp	Ile	Leu	Thr	Lys	Lys	Gly	50	55	60	
Lys	Tyr	Ile	Asp	Asn	Glu	Asn	Ile	Val	Val	Gly	Gly	Asn	Cys	Ser	Ala	65	70	75	80
Ile	Ile	Gln	Arg	Ile	Leu	Pro	Lys	Lys	Phe	Lys	Asp	Pro	Gly	Ser	Val	85	90	95	
Thr	Ile	Pro	Cys	Thr	Ile	Gly	Lys	Glu	Ala	Val	Asn	Lys	Ala	Leu	Ile	100	105	110	
Asp	Leu	Gly	Ala	Ser	Ile	Asn	Leu	Met	Pro	Leu	Ser	Met	Cys	Lys	Arg	115	120	125	
Ile	Gly	Asn	Leu	Lys	Ile	Asp	Pro	Thr	Lys	Met	Thr	Leu	Gln	Leu	Ala	130	135	140	
Asp	Arg	Ser	Ile	Thr	Arg	Pro	Tyr	Gly	Val	Val	Glu	Asp	Val	Leu	Val	145	150	155	160
Lys	Val	Arg	His	Phe	Thr	Phe	Pro	Val	Asp	Phe	Val	Ile	Met	Asp	Ile	165	170	175	
Glu	Glu	Asp	Thr	Glu	Ile	Pro	Leu	Ile	Leu	Gly	Arg	Pro	Phe	Met	Leu	180	185	190	
Thr	Ala	Asn	Cys	Val	Val	Asp	Met	Gly	Lys	Gly	Asn	Leu	Glu	Leu	Thr	195	200	205	
Ile	Asp	Asn	Gln	Lys	Ile	Thr	Phe	Asp	Leu	Ile	Lys	Ala	Met	Lys	Tyr	210	215	220	
Pro	Gln	Glu	Gly	Trp	Lys	Cys	Phe	Arg	Ile	Glu	Glu	Ile	Asp	Glu	Glu	225	230	235	240
Asp	Val	Ser	Phe	Leu	Glu	Thr	Pro	Lys	Thr	Ser	Leu	Glu	Lys	Ala	Met	245	250	255	

Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
 260 265 270

Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
 275 280 285

<210> 15
 <211> 192
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plant
 retroelement sequence

<400> 15
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 gacaaggtat ttcacgccat ctattatgct agcaaggtcc tgaatgaagc acagttgaat 120
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Glu	Val	Gln	Ala	Asp	Leu	Leu	Thr	Gln	Gly	Asn	Leu	Phe	His	Gly	Leu	85	90	95
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Asp	His	Phe	His	Gly	Leu	Leu	Arg	Lys	Thr	Pro	Thr	His	Arg	Tyr	Ser	195	200	205
Glu	Pro	Val	Gln	Leu	Asn	Ile	Phe	Ile	Asp	Asp	Leu	Gln	Leu	Leu	Ile	210	215	220
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<211> 1857

<212> DNA

<213> *Arabidopsis thaliana*

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<212> DNA

<213> *Pisum sativum*

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<213> Glycine max

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aattgggaaa agtgtcattt tatggttcga gagggcatag tcttaggcca caagatc 597
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<210> 35
 <211> 603
 <212> DNA
 <213> Glycine max

<400> 35
 tgtgataaat gtcagagAAC aaggggggata tctcgaagaa atgagatgcc tttgcagaat 60
 atcatggagg tagagatctt tgatagttag ggcatagact tcatggggcc tcttccttca 120
 tcatacagga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc 180
 atagccacgc tgaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt 240
 tcccatttgc gagtcccacg agccttgatt agtgaatggg gaacgcactt ctgcaacaat 300
 cagttgaaga aagtccctgga gcactataat gtccgacaca aggtggccac accttatcac 360
 actcagacga atggccaagc agaaatttct aacaggggagc tcaagcgaat cctggaaaag 420
 acagttgcat catcaagaaa ggattgggcc ttgaagctcg atgatactct ctgggcctat 480
 aggacagcgt tcaagactcc catcggctta tcaccatttc agctagtata tgggaaggca 540
 tgtcatttac cagtagagct ggagcacaag gcatattggg ctctcaagtt gctcaacttt 600
 gac 603

<210> 36
 <211> 150
 <212> DNA
 <213> Glycine max

<400> 36
 cctaaaatac tacaacgaca tgattggtgt tttaggataa ttgactgaaa aacctattat 60
 caatttgccg ccgttgccaa ttgggtgttt gtttgttaca tttgagattt cagacttgct 120
 tagatcaagt tcttttttcaa ttttcttttt 150

<210> 37
 <211> 11
 <212> DNA
 <213> Glycine max

<400> 37
 tggcgccggt g 11

<210> 38
 <211> 15
 <212> DNA
 <213> Glycine max

<400> 38
 tggcgccggt gccgg 15

<210> 39
 <211> 27
 <212> DNA
 <213> Glycine max

<400> 39
 tttttggcgc cggtgtcggg gatttttg 27

<210> 40
 <211> 9
 <212> DNA
 <213> Glycine max

<400> 40
 tttggggga

9

<210> 41
 <211> 16
 <212> DNA
 <213> Glycine max

<400> 41
 tttaatttgg gggatt

16

<210> 42
 <211> 775
 <212> DNA
 <213> Nicotiana tabacum

<400> 42
 gtgcgtaaag aggttttttaa actggagatt atcaagtgat tggatgccgg gggtatctac 60
 cccatttacg atagttcatg aacttctccg gtgcaatgtg tcccaaagaa ggtggcatga 120
 cgggtggtcac caatgagaag aatgagttga ttcttacaag aatggtgacc ggttggagag 180
 tgtgcatgga ctatcgcaag ctcaacaaac tcacaaggaa ggatcatttc ccatttccat 240
 tccttgacca aatgcttgat aggttggcat gtcgtgcttt ctattgcttt ctagatgtat 300
 agtcgggcta tagccaaatc tttattgctc cgtaggatca cgagaaaata cctttacatg 360
 tccttatggg acttttgcct acaagcggat gccatttggg ttgtgtaatg cactagcgaa 420
 cttttatagg tgtatgatgg ctatcttcac ggacatggg aaggactacc ttaaagtttt 480
 catggatgac ttctcgatgg ttggggattc ctttgatgat tgcttggaat atttgataa 540
 agtattggca agatatgaag aaacgaattt ggtactaaat tgggagaagt gtcatttcat 600
 gatcgaggaa ggcattgttc ttggccacaa gatctcaa atatggcattg aagtcgacaa 660
 ggcaaagatt aaggtgattt ctaaacttac acctccaact ttggtgaaag gcgtgaggag 720
 tttcttaggc cagcgggggt tttaccaatt cttcataaaa gatttcacaa aggtt 775

<210> 43
 <211> 259
 <212> PRT
 <213> Nicotiana tabacum

<400> 43
 Val Arg Lys Glu Val Phe Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala
 1 5 10 15
 Gly Val Ile Tyr Pro Ile Tyr Asp Ser Ser Glx Thr Ser Pro Val Gln
 20 25 30
 Cys Val Pro Lys Lys Gly Gly Met Thr Val Val Thr Asn Glu Lys Asn
 35 40 45
 Glu Leu Ile Pro Thr Arg Met Val Thr Gly Trp Arg Val Cys Met Asp
 50 55 60

Tyr Arg Lys Leu Asn Lys Leu Thr Arg Lys Asp His Phe Pro Phe Pro
 65 70 75 80
 Phe Leu Asp Gln Met Leu Asp Arg Leu Ala Cys Arg Ala Phe Tyr Cys
 85 90 95
 Phe Leu Asp Val Glx Ser Gly Tyr Ser Gln Ile Phe Ile Ala Pro Glx
 100 105 110
 Asp His Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Tyr
 115 120 125
 Lys Arg Met Pro Phe Gly Leu Cys Asn Ala Leu Ala Asn Phe Tyr Arg
 130 135 140
 Cys Met Met Ala Ile Phe Thr Asp Met Val Lys Asp Tyr Leu Lys Val
 145 150 155 160
 Phe Met Asp Asp Phe Ser Met Val Gly Asp Ser Phe Asp Asp Cys Leu
 165 170 175
 Glu Asn Leu Asp Lys Val Leu Ala Arg Tyr Glu Glu Thr Asn Leu Val
 180 185 190
 Leu Asn Trp Glu Lys Cys His Phe Met Ile Glu Glu Gly Ile Val Leu
 195 200 205
 Gly His Lys Ile Ser Asn Asn Gly Ile Glu Val Asp Lys Ala Lys Ile
 210 215 220
 Lys Val Ile Ser Lys Leu Thr Pro Pro Thr Leu Val Lys Gly Val Arg
 225 230 235 240
 Ser Phe Leu Gly His Ala Gly Phe Tyr Gln Phe Phe Ile Lys Asp Phe
 245 250 255
 Thr Lys Val

<210> 44

<211> 761

<212> DNA

<213> Nicotiana tabacum

<400> 44

gtgcgtaaag aggtgggtcaa gctgttggat gtcgggggttg tgtaccccat ctctgatagc 60
 tcttggactt cgccggtgca atgtgtacca aagaagggttg gcatgactgt ggtgaaaaat 120
 tccaaaaatg agttgattcc gacaagaacc atcacgggtt ggagggtatg catggactac 180
 cgcaagtga ataaagtgaac ctgcaaggat cactttcctt tgccatttct ggatcagatg 240
 ctatgacgac ttgctgggagc tgccttctat tgcttcttgg atgaatattc tgggtataac 300
 caaatcttga ttgctccgga agatccggaa aagaccacat tcaattgtcc gtatggcaca 360
 tttgttttct ctaggatgcc ttttaggttg tgtaatgcac cagctacatt tcagcgggtg 420
 atgatggcca ttttctccta tatggtgaaa gacatttttg aggtgttcat ggacgatttt 480
 agtgttgtgg ggcactcatt tgatgaatgc ttgaagaatc ttgatagggt gttggcccat 540
 tgtgaagaaa ccaatcttgt cctcaattgg gagaaatgcc actttatggt agaagaagga 600

atcaatctct ggcataaaat ttcaaaacat ggcattgagg tggataaaca aagatagatg 660
 tgatttcaag gctccctccc cctacatccg tcaagggagt ccgatgtttt cttgggcatg 720
 cggggttcta ttggagattc ataaaagact tctccaaggt t 761

<210> 45
 <211> 254
 <212> PRT
 <213> Nicotiana tabacum

<400> 45
 Val Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ser Trp Thr Ser Pro Val Gln Cys Val Pro Lys Lys
 20 25 30
 Val Gly Met Thr Val Val Lys Asn Ser Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Ile Thr Gly Trp Arg Val Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Val Thr Cys Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Glu Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Leu Ile Ala Pro Glu Asp Pro Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Phe Val Phe Ser Arg Met Pro Phe
 115 120 125
 Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Tyr Met Val Lys Asp Ile Phe Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Val Gly His Ser Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg
 165 170 175
 Val Leu Ala His Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Glu Glu Gly Ile Asn Leu Trp His Lys Ile Ser
 195 200 205
 Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
 210 215 220
 Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Cys Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Ser Lys Val

<210> 46
 <211> 762
 <212> DNA
 <213> Nicotiana tabacum

<400> 46
 gtgcgtaagg aggtgtttaa gttgttggat gttgggggttg tgtaccccat ctctgatagc 60
 tcttgcatth cgccggtgca atgtgtaccg aagaagggtg gcatgaccgt ggttgcaaat 120
 tgcgaaaatg ggttgattcc taccaggatc gtcaccgggt ggaaggatg catggattac 180
 cgaaagtgtga ataaagtgac ccgcaaggat cactttccat tgccttttct tgatcagatg 240
 ttagatcgac ttgctgggcg tgccttctac tgtttcttgg atgggtattc tggatacaac 300
 caaatcttca ttactccgga agatcaggag aagacaacat tcacttgtcc atatggcacc 360
 tttgcttttt ctaggatgcc ttttgggttg tgtaatgcac cgactacatt ctacggttat 420
 atgatggcca ttttctactga tatggtggaa gatatttttg aggtgttcat ggacgacttt 480
 agtgttgtgg gtgattcatt tgatgaatgt ttgaataatc ttgatagagt gttggcccat 540
 tgtaaagaaa ccaatcttgt tcttaattgg gagaaatgcc acttcatggt tgaggagggc 600
 atagttcttg ggcataaaaat tttaaagcat ggtatagagg tggacaaagc aaaaattgat 660
 gtgatttcaa ggctccctcc ccctacttct gtcaaggagg tgagaagttt tcttaggcac 720
 gcgggggttct accggagatt catcaaagat ttcaccaaag tt 762

<210> 47
 <211> 254
 <212> PRT
 <213> Nicotiana tabacum

<400> 47
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Val Val Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ser Cys Ile Ser Pro Val Gln Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Ala Asn Ser Gln Asn Gly Leu Ile Pro Thr
 35 40 45
 Arg Ile Val Thr Gly Trp Lys Val Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Phe Ile Thr Pro Glu Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Ser Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Tyr Met Met Ala Ile
 130 135 140

Phe Thr Asp Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Val Val Gly Asp Ser Phe Asp Glu Cys Leu Asn Asn Leu Asp Arg
165 170 175

Val Leu Ala His Cys Lys Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Glu Glu Gly Ile Val Leu Gly His Lys Ile Leu
195 200 205

Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
210 215 220

Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Arg His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 48

<211> 760

<212> DNA

<213> Nicotiana tabacum

<400> 48

gcggaaggag gtcgtcaagc tgttggtatgt cgggtgttgtg taccccatat ttgatagctc 60
ttggactttg ccggtgcaat atgtgccgaa gaaggggtgtg atgaccgtgg ttaccaatgt 120
aaaaaatgag ttgattccta ccaggactgt caccgggtgg aggggtgtgca tggattacca 180
caaattgaat aaagtgaccc gcaaggatca ctttccatta ctttttcttg atcagatgtt 240
agacagactt gctgggtgtg ctttctactg tttcttggat ggggtattctg ggtgcaacaa 300
aatTTtgatt gcaccaaag atcaggagaa gaccaccttt acttgtagct atggtacctt 360
tgtcttttct aggatgtcat ttgggttgtg taatgcaccg actacattct agaggtgtat 420
gatggccata ttacctaca tgggtggagga catTTtggag gtgtttatgg atgacttcag 480
tgttgttggg gactagtttg atgaatgttt gaaaaatctt gatagagtgt tggcccgttg 540
tgaagaagcc aaccttgtgc ttaattggga gaaatgccac ttcattggtg aggagggcat 600
agtccttagc cataaaattt caaagcatgg tatagaggtg gacaaagcaa aaattgaagt 660
gatttcaagg ctcttcccc ctacttctgt caagggagtt agaagttttc ttgggcatgc 720
ggggttctac tggagattca tcaaagactt cacgaaggtt 760

<210> 49

<211> 253

<212> PRT

<213> Nicotiana tabacum

<400> 49

Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro Ile
1 5 10 15

Phe Asp Ser Ser Trp Thr Leu Pro Val Gln Tyr Val Pro Lys Lys Gly
20 25 30

Gly Met Thr Val Val Thr Asn Val Lys Asn Glu Leu Ile Pro Thr Arg
35 40 45

Thr Val Thr Gly Trp Arg Val Cys Met Asp Tyr His Lys Leu Asn Lys
 50 55 60
 Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met Leu
 65 70 75 80
 Asp Arg Leu Ala Gly Cys Ala Phe Tyr Cys Phe Leu Asp Gly Tyr Ser
 85 90 95
 Gly Cys Asn Lys Ile Leu Ile Ala Pro Lys Asp Gln Glu Lys Thr Thr
 100 105 110
 Phe Thr Cys Thr Tyr Gly Thr Phe Val Phe Ser Arg Met Ser Phe Gly
 115 120 125
 Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Cys Met Met Ala Ile Phe
 130 135 140
 Thr Tyr Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe Ser
 145 150 155 160
 Val Val Gly Asp Glx Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg Val
 165 170 175
 Leu Ala Arg Cys Glu Glu Ala Asn Leu Val Leu Asn Trp Glu Lys Cys
 180 185 190
 His Phe Met Val Glu Glu Gly Ile Val Leu Ser His Lys Ile Ser Lys
 195 200 205
 His Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Ser Arg Leu
 210 215 220
 Leu Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Gly His Ala
 225 230 235 240
 Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 50
 <211> 762
 <212> DNA
 <213> *Oryza sativa*

<400> 50
 gtgcgtaagg aggtgtttta gttcctgtat gccaggatta tttatctcgt accatacagc 60
 gagtgggtta gccagttca ggctgtgcca aagaagggag gaatgacggc cggttgcaa 120
 gctcaaaatg aactaatccc gcaacgaacc gtaaccggat ggagaatgtg catcgattac 180
 aggaaactta acaaggctac aaaaaaggat catttcccgc tacccttcat tgatgaaatg 240
 ttggaacggc tggcaaatca ttccttcttc tgtttccttg atgggtattc aggatatcat 300
 caaattccca tccatccgga ggaccagagt aagactacgt tcacatgtcc atatggcacc 360
 tatgcgtatc gtaggatgcc ctttgactg tgcaacactc ctgcatcttt ccaaagggtgt 420
 atgatgtcta ttttctcgga catgatcgag gatatcatgg aagtcttcat ggatgacttc 480
 tcgggtctatg gaaagacttt gggtcattgt ctgcagaatc tagacaaagt cttacaacga 540
 tgccaagaaa aggacctagt gcttaactgg gaaaagtgcc atttcatggt ctgtgaaggg 600

atagttcttg ggcacgcagt gtccgaacga ggagtcgaag ttgacgcgtgc taaaattgat 660
 gtgatagatc agcttcctcc acccgtgaac atcaaaggaa tccgcagctt ctttggtcac 720
 gctggctttt atagaagggtt catcaaggac ttcacaaaag tt 762

<210> 51
 <211> 254
 <212> PRT
 <213> Oryza sativa

<400> 51
 Val Arg Lys Glu Val Phe Lys Phe Leu Tyr Ala Arg Ile Ile Tyr Leu
 1 5 10 15
 Val Pro Tyr Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Ala Val Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Thr Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Lys Thr Leu Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Cys Glu Gly Ile Val Leu Gly His Arg Val Ser
 195 200 205
 Glu Arg Gly Val Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln
 210 215 220
 Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Phe Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 52
 <211> 761
 <212> DNA
 <213> *Oryza sativa*

<400> 52
 gtgcgcaagg aggttttgaa attgctgcat gccaggatta tctatcccgt accatacagt 60
 gagagggtta gcccagtcca ggttgtgcc aagaaggag gaatggcgg cggtgcaa 120
 gctcagaatg aactaattac gcaacaaacc gtaaccgat ggaggatgtg ttcgattac 180
 aggaaactca acaaggctac aaaaaaggat catttccgc tacccttcat tgttgaaatg 240
 ttggaacggc tggcaaatca ttccttcttt tgtttccttg atggatattt cggatatcat 300
 caaattccca tccatccgga ggactagagt aagactacgt tcacatgtcc atatggcacc 360
 tatgctgcat ataggatgtc ctttggactg tgcaacgctc ctgcatcttt ccaagggtga 420
 tgatgtctat tttctcggac atgatcgagg atatcatgga agtcttcatg gatgacttct 480
 cggctctatg aaagactttc ggtcattgtc tgcaaaatct agacaaagtc ttacaacgat 540
 gccaaagaaa ggacctggtg cttaactggg aaaagtga tttcatggc cgtgaaggga 600
 tagttcttgg gcatcgagtg ttcgaacaag gaatcgaagt tgatcatgct aaaattgatg 660
 tgatagatca gcttctctct cccgtgaaca tcaaaggat ccgcagcttc ttgggtcatg 720
 tcggctttta tagaagggtc atcaaggact tcactaaagt t 761

<210> 53
 <211> 254
 <212> PRT
 <213> *Oryza sativa*

<400> 53
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Arg Ile Ile Tyr Pro
 1 5 10 15
 Val Pro Tyr Ser Glu Arg Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Ala Val Val Ala Asn Ala Gln Asn Glu Leu Ile Thr Gln
 35 40 45
 Gln Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Val Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Phe Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Glx Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr His Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140

Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Glx His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Phe
 195 200 205
 Glu Gln Gly Ile Glu Val Asp His Ala Lys Ile Asp Val Ile Asp Gln
 210 215 220
 Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 54
 <211> 762
 <212> DNA
 <213> Oryza sativa

<400> 54
 gtgcggaaag aggttttttaa gctcctgcat gccgggatta tttataccgt tccatgcagt 60
 gagggtgca gcacagtcca ggttgggccc aagatgggat gaatgacggt cggtgcaa 120
 gctcaaaata aacttatccc gcaaccaacc ataaccgat ggaggatgtg catagactac 180
 aggaaactca acaaggctac aaaagaggat ctttttccgc tacccttcat tgatgaaatg 240
 ttggaacgga tgacaaatca ttccttcttc tgtttccttg atgggtattc cggatatcat 300
 caaattccca tccgtccaga ggaccagagt aagactacgt tcacatgtcc atatggcacc 360
 tatgcgtatc gtaggatgtc ctctggactg tgcaacgctc ctgcatcttt ccaaagggtg 420
 atgttgctca ttttctcgga catgatcgaa gatatcatga aagtcttcat ggatgacttc 480
 tcagtttatg gaaagacttt cggtcattgt ctgtagaatc tagacaaagt cttacaacga 540
 tgccaagaaa atgacctagt gtttaattgg gaaaagtgcc attttatggg ccgtgaaggg 600
 atagttcttg ggcacatgat atccgaatga ggaatcgaa ttgatcgtgc taaaatcgat 660
 gttatagatc aaattcgtcc tctgcgaat atcaaaggaa tccgcagctt cttgggacat 720
 gccggccttt atagaagggt cctcaaggac ttcacaaaag tt 762

<210> 55
 <211> 254
 <212> PRT
 <213> Oryza sativa

<400> 55
 Val Arg Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Thr
 1 5 10 15
 Val Pro Cys Ser Glu Trp Val Ser Thr Val Gln Val Gly Pro Lys Met
 20 25 30
 Gly Glx Met Thr Val Val Ala Asn Ala Gln Asn Lys Leu Ile Pro Gln
 35 40 45

Pro Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Glu Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Met Thr Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr His Gln Ile Pro Ile Arg Pro Glu Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Leu Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Glu Asp Ile Met Lys Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Glx Asn Leu Asp Lys
 165 170 175
 Val Leu Gln Arg Cys Gln Glu Asn Asp Leu Val Phe Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Ser
 195 200 205
 Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln
 210 215 220
 Ile Arg Pro Pro Ala Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Leu Lys Asp Phe Thr Lys Val
 245 250

<210> 56
 <211> 762
 <212> DNA
 <213> Oryza sativa

<400> 56
 gtgcgtaagg aggtcttgaa gctcttgcac gccgagatta tttatcccgt accatataga 60
 gagtgggtta gcccgggtcta gggttatgccg aagaagggac gaatgacggt cattgcaaatt 120
 gctcaaaatg aacttattcc gcaacgaaca gtaaccggat ggaggatgtg catagattac 180
 atgaaactta acaaggctac gaaaaaggat catttcccac tacccttcat tgatgaaatg 240
 ttggaacggc tggcaaatca ttctttcttc cgtttccttg atgggtattc taggtatgat 300
 caaattccca tccatccgga ggaccaaagt aagactacgt tcacatgttc gtatgatacc 360
 tatgcttata gtaggatgtc cttcggactg tgcaacgctc ctgcatcttt ccaaagggtg 420
 atgatgtcta ttttctccga catgattaag gacattatgg aagtcttcat gcatgacttc 480
 tctatttatg gaaagacctc cggtcattgt ctacaaaatt tagacaaaat tttgcaacga 540
 tgccaagaga aggacctggt acttaattgg gaaaagtgtc atttcatggt ccgtgaaggg 600

atagttctta gtcacgcaggt gtccgaataa ggaatcgaag ttgatcgtgc taaaaactat 660
 gtaatagatt agcttccttc tctgtgaac attaagggga tccgcaattt tttgggacat 720
 gctggctttt atagaagggt catcaaagac ttcacaaagg tt 762

<210> 57
 <211> 254
 <212> PRT
 <213> Oryza sativa

<400> 57
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Glu Ile Ile Tyr Pro
 1 5 10 15
 Val Pro Tyr Arg Glu Trp Val Ser Pro Val Glx Val Met Pro Lys Lys
 20 25 30
 Gly Arg Met Thr Val Ile Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Met Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Arg Phe Leu Asp Gly Tyr
 85 90 95
 Ser Arg Tyr Asp Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Ser Tyr Asp Thr Tyr Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Lys Asp Ile Met Glu Val Phe Met His Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Lys Thr Ser Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Ile Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Arg Val Ser
 195 200 205
 Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Asn Tyr Val Ile Asp Glx
 210 215 220
 Leu Pro Ser Pro Val Asn Ile Lys Gly Ile Arg Asn Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 58
 <211> 762
 <212> DNA
 <213> Hordeum vulgare

<400> 58
 gtgcgcaagg aggttttagaa gttcctggaa gcaggatatca tctatcgtgt tgctcatagt 60
 gattggttga gtcgggtgca ttgtgtccct aagaagggag gcattaccgt tgtccctaata 120
 gataaggatg aattgatccc acagaggact attactggct ataggatggg gattgatttt 180
 aggaaattga ataaagccac taggaaagat cattaccctt tgccctttat cgaccaaagt 240
 cgagaaaggc tgtctaaaca cacacacttc tgcttttctaa acggttattt tggtttctcc 300
 caaataccag ttgcacaatc tgatcaggag aaaaccactt tcacctgccc ttttgggtaca 360
 tttgcttata gacgtatgac ttttggctta tgtaatgcac ctgcctcctt tcaaagatgt 420
 atgatggcta tattccctga cttttgtgaa aagattgttg aggttttcat ggatgacttc 480
 tccattttacg gatcttcctt tgatgattgc ctcagcaacc ttgatcgagt cttgcagaga 540
 tgtaaagaca ccaatctttt cttgaattgg aagaagtgcc actttatggg taatgacggc 600
 atcgtcttag gacataaatt ttctgaaaga ggtattgaag tcgataaggc taagggttgat 660
 ggaatcgaga aaatgccata cccacagat atcaaaggga taagaagttt ccttggtcat 720
 gctggtttct atagaagggt cataaaagac ttcactaagg tt 762

<210> 59
 <211> 254
 <212> PRT
 <213> Hordeum vulgare

<400> 59
 Val Arg Lys Glu Val Glx Lys Phe Leu Glu Ala Gly Ile Ile Tyr Arg
 1 5 10 15
 Val Ala His Ser Asp Trp Leu Ser Arg Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Arg Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asn Gly Tyr
 85 90 95
 Phe Gly Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Thr Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140

Phe Pro Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Phe Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Asn Asp Gly Ile Val Leu Gly His Lys Phe Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Gly Ile Glu Lys
 210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 60
 <211> 762
 <212> DNA
 <213> Hordeum vulgare

<400> 60
 gtgcgtaaag aggtcctaaa gttcctggaa gcgggtatta tctatcctgt tgctcacaac 60
 gattgggtga gtccggtgca ttgcgtccct aagaagggat gcattaccgt tgtccctaata 120
 gataaggatg aattgatccc acataggatt attactggct ataggatggg gatcgatttt 180
 agggaaatga ataaagccac taggaaagaa cattaccctt tgccttttag cgaccaaata 240
 ctagaaagggt tgtctaaaca cacacacttc tgctttctag acggttattc tagtttctcc 300
 caaatactag ttgcacaatc tgatcaggag aaaaccactt tcacctaccg gttcgggtacc 360
 tttgcttata gacgtatgcc ttttggctta tgtaatgcac ctgccacctt tcaaagatgt 420
 atgatggcta tattctctga cttttgtgaa aagtttgtcg aggttttcat ggatgacttt 480
 tccgtttacg gatcttccct tgatgattgc ctcaacaacc ttgatcgggt cttgcagaga 540
 tgtaaagata ctaatcttgt cttgaattgg gagaagtgcc actttatggt taatgaaggc 600
 atcgtcttag gacataaaat ttccgaaaga ggtattgaat tcgataaggc taaggttggg 660
 gcaatcaaga aaatgccata cccacagat atcaaaggta taagaagttt cttggtccat 720
 gctggtttct atagaagggt catcaaggac ttacaaagg tt 762

<210> 61
 <211> 254
 <212> PRT
 <213> Hordeum vulgare

<400> 61
 Val Arg Lys Glu Val Leu Lys Phe Leu Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala His Asn Asp Trp Val Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Cys Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro His
 35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Met Asn
50 55 60

Lys Ala Thr Arg Lys Glu His Tyr Pro Leu Pro Phe Ser Asp Gln Met
65 70 75 80

Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Ser Phe Ser Gln Ile Leu Val Ala Gln Ser Asp Gln Glu Lys Thr
100 105 110

Thr Phe Thr Tyr Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
130 135 140

Phe Ser Asp Phe Cys Glu Lys Phe Val Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Asn Asn Leu Asp Arg
165 170 175

Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
195 200 205

Glu Arg Gly Ile Glu Phe Asp Lys Ala Lys Val Gly Ala Ile Lys Lys
210 215 220

Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Val His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 62

<211> 757

<212> DNA

<213> Hordeum vulgare

<400> 62

gaaaagaggt tgtgaagctc ctggatgaag gtattatcta tcatgttgct catagcgatt 60
gggtgagtc ggtgcatagc gttcctaaga agggaggcat taccgttgtc cctaatagata 120
aggatgaatt gatcccgagc aggattatca ctggctatag gatggtgatc gatttcagga 180
aactgaataa agccactagg aaagatcatt accctttgcc ttttatcgac catatgctag 240
aaaggttgtc caaactcaca cacttctgct ttctagacgg ttattctagt ttctccaaa 300
taccagttgc acaatctgat caggagaaaa ccactttcac ctgccctttc ggtacctttg 360
cttatagacg tatgcctttt ggcttatgta atgcacctgc cacctttcaa agatgtatga 420
tggtatatt ctctaacttt tgtgaaaata ttgtcgaggt tttcatggat gacttttccg 480
tttacgggtc ttcttttgat gattgcctca gcaaccttga tcgagtctta cagagatgta 540
aagacaccaa tcttgtcttg aatggggaga agtgccactt tatgtttaat gaaggcatcg 600

tcttaggaca taaaatttct gaaagaggta ttgaagtcga taaggctaag gttgatgcaa 660
 tcgacaaaat gccatacccc acagatatca aagggtataag aagtttcctt gggtcatgggtg 720
 gtttctatag aaggtttatc aaagatttca caaagggt 757

<210> 63
 <211> 251
 <212> PRT
 <213> Hordeum vulgare

<400> 63
 Lys Glu Val Val Lys Leu Leu Asp Glu Gly Ile Ile Tyr His Val Ala
 1 5 10 15
 His Ser Asp Trp Val Ser Pro Val His Ser Val Pro Lys Lys Gly Gly
 20 25 30
 Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln Arg Ile
 35 40 45
 Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn Lys Ala
 50 55 60
 Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp His Met Leu Glu
 65 70 75 80
 Arg Leu Ser Lys Leu Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser
 85 90 95
 Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr Thr Phe
 100 105 110
 Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu
 115 120 125
 Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile Phe Ser
 130 135 140
 Asn Phe Cys Glu Asn Ile Val Glu Val Phe Met Asp Asp Phe Ser Val
 145 150 155 160
 Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg Val Leu
 165 170 175
 Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Gly Glu Lys Cys His
 180 185 190
 Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser Glu Arg
 195 200 205
 Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Asp Lys Met Pro
 210 215 220
 Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His Gly Gly
 225 230 235 240
 Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys

<210> 64
 <211> 740
 <212> DNA
 <213> Hordeum vulgare

<400> 64
 gtgcgtaaag aggtgattaa attcctagaa gaaggtatta tctatcctgt tgctcacagc 60
 gattgggtga gtccggtgca ttgcattcct aagaaaggag gcattaccgt tgccctaata 120
 gataaggatg aattgatccc atagaggatt attactggct ataggatggg gattgatttt 180
 aggaagttga ataaagccac taggaaagat cattaccctt tgccttttat cgaccaaagt 240
 ctagaaaggc tgtctaaaca cacacacttc ttgtttctgg acggttatac tggtttctcc 300
 caaataccag ttgcacaatt tgatcaggag aaaaccactt taacctgaca tttcgggtacc 360
 tttgcttata tacgtatgcc ttttggcttg tgtaatgcac ctgccacctt tcaaagatgt 420
 atgatggcta tattctccga cttctgtgaa aagattgtca atgttttcat ggataacttc 480
 tccgttttac ggtgttcctt tgatgattgc ctcaacaacg ttgatcgagt cttacagaga 540
 tgtaaggaca ccaatgttgt cttgaattgg gagaagtgtc actttatggg taatgaaggc 600
 atcgtcttag gacataagat ttctgaaaga ggtattaaag ttgataaggc taagggtgat 660
 gcaatcgaga aaatgccata tccacagata tcaaagggtat aagaagtttc cttggtcatg 720
 ctggtttcta tagaaggttc 740

<210> 65
 <211> 247
 <212> PRT
 <213> Hordeum vulgare

<400> 65
 Val Arg Lys Glu Val Ile Lys Phe Leu Glu Glu Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala His Ser Asp Trp Val Ser Pro Val His Cys Ile Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Glx
 35 40 45
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Lys His Thr His Phe Leu Phe Leu Asp Gly Tyr
 85 90 95
 Thr Gly Phe Ser Gln Ile Pro Val Ala Gln Phe Asp Gln Glu Lys Thr
 100 105 110
 Thr Leu Thr Glx His Phe Gly Thr Phe Ala Tyr Ile Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Val Asn Val Phe Met Asp Asn Phe
145 150 155 160

Ser Val Tyr Gly Cys Ser Phe Asp Asp Cys Leu Asn Asn Val Asp Arg
165 170 175

Val Leu Gln Arg Cys Lys Asp Thr Asn Val Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
195 200 205

Glu Arg Gly Ile Lys Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
210 215 220

Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe
245

<210> 66
<211> 762
<212> DNA
<213> Avena sativa

<400> 66
gtgcgaaagg aggttttcaa gtcctatggat gctgggtatta tttaccctat tgctgatagt 60
gaatgggtta gtcctatgta ttgtgttcct aaaaaggagg gtattaccgt tgcctcta 120
gataatgatg agcttattcc tcaaagaata gtggtaggct ataggatgtg catcgatttt 180
aggaaagtca ataaagttac taagaaagat cactaccgc ttccttttat tgatcaaagt 240
ttggaaagat tttctaaaaa gacccatttt tgttttcttg atggttattc tggtttctct 300
caaattgttg ttaaacaaca agatcaagaa aaaactactt ttacttgccc ttatggaact 360
tatgcttata gatgtatgcc ttttggttta tgtaatgctc cttctacttt cctaagggtgc 420
atgtctgcta tctttcatgg tttttgtgag gaaattgtag aagtgttcat ggacgacttt 480
tctgtctacg gaacttcttt tgataattgt ctgcacaacc ttgataaagt tttacagaga 540
tgtgaaggaa ctaattctgt tcttaattgg gagaaatgcc acttcattgg taatgaaggg 600
attgttcttg ggcataaagt ttctaaaaga ggcatagaag ttgatagagc taagggtgag 660
gcaattgaga agatgccatg tccaagagac atcaaaggta ttcgtagtat ccttggtcat 720
gctggtttct ataggagggt catcaaagac ttcacaaagg tt 762

<210> 67
<211> 254
<212> PRT
<213> Avena sativa

<400> 67
Val Arg Lys Glu Val Phe Lys Leu Met Asp Ala Gly Ile Ile Tyr Pro
1 5 10 15
Ile Ala Asp Ser Glu Trp Val Ser His Val His Cys Val Pro Lys Lys
20 25 30
Gly Gly Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln
35 40 45

Arg Ile Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn
50 55 60

Lys Val Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
65 70 75 80

Leu Glu Arg Phe Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Gly Phe Ser Gln Ile Val Val Lys Gln Gln Asp Gln Glu Lys Thr
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Cys Met Pro Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ser Thr Phe Leu Arg Cys Met Ser Ala Ile
130 135 140

Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys
165 170 175

Val Leu Gln Arg Cys Glu Gly Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
195 200 205

Lys Arg Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys
210 215 220

Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 68

<211> 762

<212> DNA

<213> Avena sativa

<400> 68

gtgcgcaaag aggtctttta gttccttgat gctgggtatta tttaccctat tgctgatagt 60
caatgggtta gccttggtca ttgtgtcccc aagaaagggg gaataactgt tgtgcctaata 120
gaagataatg agcttatacc ccaaagagta gtgggttggt atagaatgtg cattgatatt 180
agaaggatta ataaagttac taggaaagat cattatcctt tgccctttat tgatcaaagt 240
cttgagaggt tgtccaaaaa gactcacttt tgttttcttg atggtcattc tgggttttct 300
caaattgttg tgaaagcaca agaccaagag aaaactactt tcacttggtc ttatgggtact 360
tatgattata ggcgtatgcc ttttggttta tgtaatgctc ctgctacatt tcagagatgt 420
atgtctgcta tatttcatgg tttttgtgaa gaaattgtgg aggttttcat ggacgatatt 480
tctgtctatg gaacttcttt tgataactgt ttgcacaacc ttgataaatt tttgcagaga 540
tttgaagaaa ccaaccttgt tcttaattgg gagaaatgcc atttcatggt taatgaaggg 600

attgttcttg gacacaagat ctcagaaaga ggcattgaag ttgacagagc caaaattgaa 660
gcaattgaga acatgccttg ccctagagat attaaaggta ttcgtagtat ccttggtcat 720
gctggtttct atagtaggtt catcaaagac ttacaaaag tt 762

<210> 69
<211> 254
<212> PRT
<213> Avena sativa

<400> 69
Val Arg Lys Glu Val Phe Lys Phe Leu Asp Ala Gly Ile Ile Tyr Pro
1 5 10 15
Ile Ala Asp Ser Gln Trp Val Ser Leu Val His Cys Val Pro Lys Lys
20 25 30
Gly Gly Ile Thr Val Val Pro Asn Glu Asp Asn Glu Leu Ile Pro Gln
35 40 45
Arg Val Val Val Val Tyr Arg Met Cys Ile Asp Phe Arg Arg Ile Asn
50 55 60
Lys Val Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
65 70 75 80
Leu Glu Arg Leu Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly His
85 90 95
Ser Gly Phe Ser Gln Ile Val Val Lys Ala Gln Asp Gln Glu Lys Thr
100 105 110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Asp Tyr Arg Arg Met Pro Phe
115 120 125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ser Ala Ile
130 135 140
Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe
145 150 155 160
Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys
165 170 175
Phe Leu Gln Arg Phe Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
195 200 205
Glu Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Glu Ala Ile Glu Asn
210 215 220
Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His
225 230 235 240
Ala Gly Phe Tyr Ser Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 70
 <211> 756
 <212> DNA
 <213> Avena sativa

<400> 70
 aaggagggttt ttaaactcct tgatgttgggt attattttacc ctattgctga tagtgaatgg 60
 gttagtcttg ttcattgtgt tcctaaaaag ggaggtatta ccgttggtcc taatgataat 120
 gatgagctta ttcctcaaag aatagtggta ggctatagga tgtgcataga ttttaggaaa 180
 gttaataaag ttactaagaa agatcactac ccgcttcctt ttattgatca aatgttggaa 240
 aggttgtcta aaaagaccca tttttgtttt cttgatgggt actctagctt ctctcaaatt 300
 gctgtttaaac aacaagatca agaaaaaact acttttactt gcccttatgg aacttttgct 360
 tatagacgta tgcctattgg tttatgtaat gctcctgcta cttttcaaag gtgtatgtct 420
 gctatatctt atgggttttg tgaggaaatt gtagaagtgt tcatggatga cttttctgtc 480
 tatggaactt cttttgataa ttgcctgcac aaccttgata aagttttgca gagatgtgaa 540
 gaaactaata ttgttcttaa ttgggagaaa ttccacttca tggttaatga agggattgtc 600
 cttgggcata aagtttctaa aagaggcata gaagttgata gagctaaggt tgaggcaatt 660
 gagaagatgc catgcccaag agacatcaaa ggtatacgtg gtatccttgg tcatgctggt 720
 ttctatagaa ggtttatcaa agacttcaca aaggtt 756

<210> 71
 <211> 252
 <212> PRT
 <213> Avena sativa

<400> 71
 Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro Ile Ala
 1 5 10 15
 Asp Ser Glu Trp Val Ser Leu Val His Cys Val Pro Lys Lys Gly Gly
 20 25 30
 Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln Arg Ile
 35 40 45
 Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn Lys Val
 50 55 60
 Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met Leu Glu
 65 70 75 80
 Arg Leu Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser
 85 90 95
 Phe Ser Gln Ile Ala Val Lys Gln Gln Asp Gln Glu Lys Thr Thr Phe
 100 105 110
 Thr Cys Pro Tyr Gly Thr Phe Ala Tyr Arg Arg Met Pro Ile Gly Leu
 115 120 125
 Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ser Ala Ile Phe His
 130 135 140

Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe Ser Val
 145 150 155 160

Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys Val Leu
 165 170 175

Gln Arg Cys Glu Glu Thr Asn Ile Val Leu Asn Trp Glu Lys Phe His
 180 185 190

Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser Lys Arg
 195 200 205

Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys Met Pro
 210 215 220

Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His Ala Gly
 225 230 235 240

Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 72

<211> 748

<212> DNA

<213> Secale cereale

<400> 72

gtgcggaag aggtctttta actcctagag gcaggtatta actatcccat tgctgatagc 60
 cagcggttaa gtcattgtcca ttgtgttcct aagaaaggag gtatgactgt cgtccctaag 120
 gataaagatg aatttatccc gcaaagaata gttacagggt ataggatggt aattgatttt 180
 cgtaagttaa ataaagctac tatgaaagat cattaccctt tgccatttat tgatcaaagt 240
 ccagacaggt tatccaaaca tactcatttc tgctttctag atggttattc tggtttctct 300
 caaatacctt tgtcaaaggg ggatcaagaa aagaccacct ttacttgctc ttccggtacc 360
 tttgcttata gaggtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgt 420
 atgatcgtaa tattctctgt cttttttgaa aagattggtg aggtattcat ggatgatttc 480
 tccggttatg gaacttcttt tgatgattgc ttaagcaacc ttgatcgagt ttgcagaga 540
 tgtgaagata ctaaccttgt cttgaattgg gagaagtgcc actttatggt taatgaaggc 600
 attttcttgg gacataaaat ttctgaaaga ggtactgaag ttgagaaagc taaagtggat 660
 gctattgaaa agatgccatg ccctaaggat atgaaaggta tacgaagttt ccttggtcac 720
 gctgggtttt ataggaggtt cataaaag 748

<210> 73

<211> 249

<212> PRT

<213> Secale cereale

<400> 73

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Asn Tyr Pro
 1 5 10 15

Ile Ala Asp Ser Gln Arg Val Ser His Val His Cys Val Pro Lys Lys
 20 25 30

Gly Gly Met Thr Val Val Pro Lys Asp Lys Asp Glu Phe Ile Pro Gln
 35 40 45

Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Met Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Pro Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Phe Ser Gln Ile Pro Leu Ser Lys Gly Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Gly Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ile Val Ile
 130 135 140
 Phe Ser Val Phe Phe Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Phe Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Thr Glu Val Glu Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Pro Cys Pro Lys Asp Met Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys
 245

<210> 74
 <211> 762
 <212> DNA
 <213> Secale cereale

<400> 74
 gtgcggaagg aggtcggttaa gcttccagag gcagggtatta tctatcccgt tgctgatagc 60
 cagtgggttaa gtcattgtcca ttgtgtccct aagaagggag gtatgactgt cggttcctaat 120
 gacaaacatg aattgatccc gcaaagaata gttacagggt ataggatggt aattgatttc 180
 cgtaagttaa ataaagctac taagaaagat cattaccctt tgccatttat tgatcaaagt 240
 ctgacaggt tatccaaaaca tactcatttt tgctttctag atggttatta tggtttctct 300
 caaataacctg tgtcaaaagg ggatcaagaa aagaccactt tcaattgtcc tttcgggtacc 360
 tttgcttata gacgtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgt 420
 atgatggcta tattatctga tttttgagaa aagattgttg aggttttcat ggatgatttc 480
 tccgtttacg gaacttcttt tgatgactac ttaagcaaca atgatcgagt tttgcagaga 540
 tgtgaagaca ctaatcttgt tttgaattgg gagaagtgcc actttatggt taatgaaggc 600

attgtcttgg gacaaaaaat ttctgaaaga ggtattgaag ttgacaaagc taaagtcgat 660
 gctgttgaaa agatgccatg ccccaaggac atcaaaggta tacgaagttt ccttggtcat 720
 gttgggtttt ataggagggtt catcaaagac ttcacgaaag tt 762

<210> 75
 <211> 254
 <212> PRT
 <213> Secale cereale

<400> 75
 Val Arg Lys Glu Val Val Lys Leu Pro Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Gln Trp Val Ser His Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Pro Asn Asp Lys His Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Tyr Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Leu Ser Asp Phe Glx Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asp Tyr Leu Ser Asn Asn Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly Gln Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Val Glu Lys
 210 215 220
 Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 76
 <211> 762
 <212> DNA
 <213> Secale cereale

<400> 76
 gtgcgtaagg aggtgggttaa gtccttagaa gcagggtatta tctatccagt tgctgatagt 60
 cagtgggttaa gtcattgtcca ttatgttcct aagaaaggag gtatgactgt tgtccctaata 120
 gataaagatg aattgatccc gcaaagaata gttacagggt ataggatggg aagtgatttc 180
 cgtaagttga ataaagccac taagaaagat cattaccctt tgccatttat tgatcaaagt 240
 ctagaaagggt tatccaaaca tactcatttc ttctttctag atggttattc tggtttctct 300
 caaatacctg tgtcaaaagg ggatcaagaa aagaccacct ttacttgtag ttccgggtacc 360
 tttgcttata gacgtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgc 420
 atgatggcta tattctctga cttttgtgaa aagattgttg aggtattcat ggatgatttc 480
 tccgttttac gaacttcttt tgatgattgc ttaagcaacc ttgatcgagt tttgcagaga 540
 tgtgaagaca ctaaccttgt cttgaattgc gagaagtgcc actttatggg taatgaaggc 600
 attgtcttgg gacataaaat ttctgaaata ggtattgaag ttgacaaagc taaagttgat 660
 gctattgaaa agatgccatg cgcaaaggac atcaaaggta tacggagttt ccttggtcat 720
 gccgggtttt ataggaggtt catcaaagat ttctcaaagg tt 762

<210> 77
 <211> 254
 <212> PRT
 <213> Secale cereale

<400> 77
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Gln Trp Val Ser His Val His Tyr Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Thr Gly Tyr Arg Met Val Ser Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Lys His Thr His Phe Phe Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Thr Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
165 170 175

Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Cys Glu Lys
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
195 200 205

Glu Ile Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
210 215 220

Met Pro Cys Ala Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
245 250

<210> 78

<211> 759

<212> DNA

<213> Secale cereale

<400> 78

gtgcgcaagg aagtttttaa gtttctagag gcaggtataa tctatccagt tgctgatagc 60
cagtgggttaa gtcctgtcca ttgtgtccct aagaaggag gtatgactgt agttcctaata 120
gataaagatg aattgatctc gcaaagaatt gttacagggt ataggatggt aattgatttt 180
cgcaaattaa ataaagccac taagaaagat caataccctt tgccttttat tgatcaaagt 240
ctagaaaagg tatccaaaca caccattttt tgcttttctag atggttattc tagtttctct 300
caaataccta tgtcaaaagg ggataaagaa aagaccactt ttacttgtcc ctttggtact 360
ttgcttatag acgtatgctt tttggtttat gtaatgcata tgctaccttt caaacatgca 420
tgatggctat actctatgat ttttgtgaaa gaatgttgat gttttcatgg atgatttttg 480
tatttacgaa acttcttttg atgattgctt gagcaacctt gatcgagttt tgcagagatg 540
tgaagaaact aatcttgtct tgaactggga aaagtccac tttatgggta atgaaggcat 600
tgcttgggac ataaaatttc tgaaagaggt accgaagttg acaaagctaa agttgatgct 660
gttgaaaaga tgccatgtcc caaggacatc aaaggtataa gaagtttctt tggatcatgcc 720
gggttttata ggaggtttat caaggacttc accaagggtt 759

<210> 79

<211> 254

<212> PRT

<213> Secale cereale

<400> 79

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Ile Tyr Pro
1 5 10 15

Val Ala Asp Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys
20 25 30

Gly Gly Met Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Ser Gln
35 40 45

Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp Gln Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Ser Phe Ser Gln Ile Pro Met Ser Lys Gly Asp Lys Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Ser Ala Thr Phe Gln Thr Cys Met Met Ala Ile
 130 135 140
 Leu Tyr Asp Phe Cys Glu Arg Ile Val Asp Val Phe Met Asp Asp Phe
 145 150 155 160
 Cys Ile Tyr Glu Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Ser His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Thr Glu Val Asp Lys Ala Lys Val Asp Ala Val Glu Lys
 210 215 220
 Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 80

<211> 761

<212> DNA

<213> Triticum aestivum

<400> 80

gtgcgtaagg aggttctcaa gtttctggag gtaggtataa tttatcccgt tgctgatagt 60
 cagtgggtaa gtccgtgcc tttgtgccct aagaaggagg gtattactgt tgccctaatt 120
 gataaagatg aattgattcc tcaaagaatt attacgggta taggatggta attgatttcc 180
 gcaaattaaa taaagccact aagagagatc attacccctt accttttatt gatcaaattc 240
 tagaaagatt atgcaaacat acacattatt gcttccaaga tggttatcct gggttttctc 300
 aaatacctgt gtcggctaaa gatcaatcaa agactacttt tacatgccct tttgggtactt 360
 ttgcttatag atgtatgcct tttggtttat gtaatgcacc tgctaccttt caaagatgca 420
 tgatggctat attctctgat ttttgtgaaa agatttgtga gggtttcatg gatgactttt 480
 ccgtctatgg ttctcttttt gatgattgct tgagcaatct tgatcgagtt ttgcagagat 540
 gtgaagaaac taatcttgtc ttgaattggg aaaagtgtca ctttatgggt aatgaaggta 600

ttgtcttggg gcacaaagtt tctgaaagag gtattgaagt tgataaagcc aaggttgaca 660
 ctattgaaaa gataccatgt cccaaggaca tcaaaggtag aagaagtttc cttgggtcacg 720
 ccggatttta taggaggttc ataaaagatt tcacaaaggt t 761

<210> 81
 <211> 254
 <212> PRT
 <213> Triticum aestivum

<400> 81
 Val Arg Lys Glu Val Leu Lys Phe Leu Glu Val Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Arg Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Ile
 65 70 75 80
 Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Gln Asp Gly Tyr
 85 90 95
 Pro Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Thr Ile Glu Lys
 210 215 220
 Ile Pro Cys Pro Lys Asp Ile Lys Gly Thr Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 82
 <211> 780
 <212> DNA
 <213> Triticum aestivum

<400> 82
 gtgcggaagg aggtgtttaa gtccttgag gcaggataaa tttatcccgt tgctgatagt 60
 aagtgggtaa ttcctgtcca ttaagtgatc gtgattactg ttgttcctaa gaagggaggt 120
 attaccgttg ttcctaataa taaagatgaa ttgattcctc aaagaaccat tactgggtat 180
 aggatggtaa ttgatttccg caaattaaat aaggctacta aaaaatatca ttaccoccta 240
 ccttttatcg atcaaagtct agaaagatta tccaaacata cacatttttg ctttctagat 300
 ggttactctg gtttctctca aatacctgtg tcagccaaag atcaatcaaa gactactttt 360
 acatgccctt ttggtacttt tgcttataga cgtatgcctt ttggtttatg taatgcacct 420
 gctacctttc aaagatacat gatggctata ttatctgact tttgtgaaaa gatttgtgag 480
 gttttcatgg acgactcttc catctatgga tcttcttttg atgattgctt gagcaacctt 540
 gatcgagttt tgcagagatg tgaagaaact tatcttgtct tgaattggga aaagtgccaa 600
 tttatgggta atgaaggatg tgctctgggg cataaagttt ctgaaagagg tattcgagtt 660
 gataaagcca aggttgatgc tattgaaaag atgccatgtc ccatggacat caaagggtata 720
 agaagtttcc ttggtcatgc cggtttttat aggaggttca taaaagactt cacgaagggt 780

<210> 83
 <211> 260
 <212> PRT
 <213> Triticum aestivum

<400> 83
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Lys Trp Val Ile Pro Val His Glx Val Ile Val Ile
 20 25 30
 Thr Val Val Pro Lys Lys Gly Gly Ile Thr Val Val Pro Asn Asp Lys
 35 40 45
 Asp Glu Leu Ile Pro Gln Arg Thr Ile Thr Gly Tyr Arg Met Val Ile
 50 55 60
 Asp Phe Arg Lys Leu Asn Lys Ala Thr Lys Lys Tyr His Tyr Pro Leu
 65 70 75 80
 Pro Phe Ile Asp Gln Met Leu Glu Arg Leu Ser Lys His Thr His Phe
 85 90 95
 Cys Phe Leu Asp Gly Tyr Ser Gly Phe Ser Gln Ile Pro Val Ser Ala
 100 105 110
 Lys Asp Gln Ser Lys Thr Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala
 115 120 125
 Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln
 130 135 140

Arg Tyr Met Met Ala Ile Leu Ser Asp Phe Cys Glu Lys Ile Cys Glu
145 150 155 160

Val Phe Met Asp Asp Ser Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys
165 170 175

Leu Ser Asn Leu Asp Arg Val Leu Gln Arg Cys Glu Glu Thr Tyr Leu
180 185 190

Val Leu Asn Trp Glu Lys Cys Gln Phe Met Val Asn Glu Gly Ile Val
195 200 205

Leu Gly His Lys Val Ser Glu Arg Gly Ile Arg Val Asp Lys Ala Lys
210 215 220

Val Asp Ala Ile Glu Lys Met Pro Cys Pro Met Asp Ile Lys Gly Ile
225 230 235 240

Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp
245 250 255

Phe Thr Lys Val
260

<210> 84

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 84

gtgcgtaagg aggtattcaa gcttctggag gcaggtataa tttatcccgt tgttgatagt 60
caatgggtaa gtcctgtcca ttgtgtcctt aagaaggag gtattactgt tgtccctaatt 120
gataaagatg aattgattcc gcaaagaatt atcacagggt ataggatggt aattgatttc 180
cgtaagttaa ataaagctac taagaaagat cattaccctt taccttttat tgatcaaattg 240
ttagaaagat tatgcaaaca tacacattat tgctttctag atggttattc tggtttctct 300
caaatacctg tgtcagctaa ggatcaatca aagactactt ttacatgccc ttttggtact 360
tttggttata gacgtatgcc tttcgattta tgtaatgcac ctgctacctt tcaaatatgc 420
atgatggcta tattctctga cttttgcgaa aagatttgtg aggttttcat ggacgacttt 480
tccgtctatg gttcctctta tgatgattgc ttgagcaatc ttaatcgagt tttgcagaga 540
tgtgaagaaa ctaatcttgt cttgaattgg gaaaagtgcc actttatggt taatgaagg 600
attgtcttgg ggcacaaaagt ttctgaacga ggtattgaag ttgataaggc caaggttgat 660
gctattgaaa agatgacatg tcccaaggac atcaaaggta taagaagttt ccttggtcac 720
gccagatttt ataggagggt cataaaagac ttcacaaagg tt 762

<210> 85

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 85

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro
1 5 10 15

Val Val Asp Ser Gln Trp Val Ser Pro Val His Cys Val Leu Lys Lys
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Gly Tyr Arg Arg Met Pro Phe
 115 120 125
 Asp Leu Cys Asn Ala Pro Ala Thr Phe Gln Ile Cys Met Met Ala Ile
 130 135 140
 Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Ser Ser Tyr Asp Asp Cys Leu Ser Asn Leu Asn Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Thr Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 86
 <211> 762
 <212> DNA
 <213> Triticum aestivum

<400> 86
 gtgcggaaag aggtgctcaa gcttctggag gcaggataaa tttatcccgt tgctgagagt 60
 cagtgggttaa gtcctgtcca ttgtgtccct aagaaggag gtattactgt tgtccctaata 120
 gataaagatg aattgattcc tcaaagaatt attacagggt ataggatggt aattgatttc 180
 cgcaaattaa ataaagccac caagaaagat cattaccctt taccttttat tgatcaaatg 240
 ctagaaagat tatgcaaaca tacacattat tgcttcctag atgggtattc tgggtttctct 300
 caaataacctg tgtcgggctaa agatcaatca aagactactt ttacatgcc ttttgggtact 360
 tttgcttata gacgtatgcc ttttggttta tgtaatgcac cttctacctt tcaaagatgc 420

atgatggcta tattctctga tttttgtgaa aagatttgtg aggttttcat ggacgaattt 480
 tccgtctatg gttcctcttt tgatgattgc ttgagcaatc ctgatcgagt tttgcagaga 540
 tgtgaagaaa ctaatcttgt cttgaattgg gaaaagtgcc actttatggt taatgaaggt 600
 attgtcttgg ggcacaaaagt ttctgaaaga ggtattgaag ttgataaagc caagggtgac 660
 gctattgaaa agatgccatg tcccaaggac atcaaaggta taagaagttt ccttggtcac 720
 gccgatttt ataggagggt cataaaagac ttcacaaagg tt 762

<210> 87

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 87

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15

Val Ala Glu Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60

Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80

Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95

Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr
 100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Ser Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Glu Phe
 145 150 155 160

Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Pro Asp Arg
 165 170 175

Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220

Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His

225

230

235

240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 88

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 88

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gtgCGtaagg aggttttcaa gttccttgag gcaggTatta cttatcccgt tgctgatagt 60
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gataaagatg aattgatccc gcaaataatt attacagggt ataggatggt aattgatttc 180
cataagttaa ataaagctac taagaaagat cattaccctt tacctcttat tgatcaaatt 240
ctagaaagac tatccaaaca cacacatttc tgctttctag atgggtatac tgggtttctct 300
caaatacctg tgtcagtga ggaatcaatct aaaactactt ttacttgccc ttttggtact 360
tttgcttata gacttatgcc ttttggttta tgtaatgcac ctacttcctt tcaaagatgc 420
atgatggcta tattctctgt tttttgtgaa aatatttgtg aggtattcat ggatgatttc 480
tccgtttatg gatcctcttt tgatgattgt ttgagcaacc ttgatcgagt tttgcagaga 540
tgCGaagaca ctagtctcat cctgaattgg gaaaagtgtc actttatggt taatgaaggc 600
attgtcttgg ggcataagat ttccgagaga ggtattgaag ttgacaaagc caaagttgat 660
gctattgaaa agattccatg tccaaggac ataaaaggta taagaagttt ccttggtcat 720
gctggttttt ataggaggtt catcaaagac ttctcaaagg tt 762

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<210> 89

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 89

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Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Thr Tyr Pro
  1              5              10              15

Val Ala Asp Ser Glu Trp Val Ser Pro Leu His Cys Val Pro Lys Lys
      20              25              30

Gly Gly Ile Thr Val Val Leu Asn Asp Lys Asp Glu Leu Ile Pro Gln
      35              40              45

Ile Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe His Lys Leu Asn
      50              55              60

Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Leu Ile Asp Gln Ile
      65              70              75              80

Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
      85              90              95

Thr Gly Phe Ser Gln Ile Pro Val Ser Val Lys Asp Gln Ser Lys Thr
      100              105              110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Leu Met Pro Phe
      115              120              125

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Gly Leu Cys Asn Ala Pro Thr Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140

Phe Ser Val Phe Cys Glu Asn Ile Cys Glu Val Phe Met Asp Asp Phe
 145 150 155 160

Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175

Val Leu Gln Arg Cys Glu Asp Thr Ser Leu Ile Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220

Ile Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 90

<211> 791

<212> DNA

<213> *Gossypium hirsutum*

<400> 90

gtgcgcaagg aggtttttaa gctacttgat gacgggatga tctatcccat atctaacagt 60
 aattgggtta gccagtaga catagtaga aaaaagacca gtgcaaccgt aatcgagaat 120
 tcggcagggt agatagttcc cactcgggtc caaaacgggt ggagagtagt catcgattac 180
 aggaagtga attccttaac tcggaaggat cactttccac ttctttttat tgaccagatg 240
 ttagaacgtt tagctggaaa gtctcattat ttagaacgtt tagctggaaa gtctcattat 300
 tgttggttg atggttacta aggttttttc cagatcccag tggcaccgga ggatcaagaa 360
 agacaatgtt tacgtgccc a ttggcacgt tttcttacag acggatgccg ttcggactct 420
 gtaatgcacc agccagtttt cataggtgca tggtaagtat attttcagac tacgtcgata 480
 aaattatcga ggtgttcatt gacgacttta ctgtatatgg tgagtccttc gaggttaagt 540
 tgacgaacct tgcaaaaatt ttggaaagat gcttagaatt taatcttggt ctaaattatg 600
 agaaatgcc a ttttatggta gacaaggat tagttctagg tcatattatt tctgctgatg 660
 gaatttctgt tgataaagca aaaatcaaca tcattaactc actaccatac cccacaactg 720
 tgaggagat ttggtcttct cttggtcatg caggtttcta caagtgggtc atcaaagact 780
 tttcaaaagt t 791

<210> 91

<211> 264

<212> PRT

<213> *Gossypium hirsutum*

<400> 91

Val Arg Lys Glu Val Leu Lys Leu Leu Asp Asp Gly Met Ile Tyr Pro
 1 5 10 15

Ile Ser Asn Ser Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys

20										25										30																																		
Thr	Ser	Ala	Thr	Val	Ile	Glu	Asn	Ser	Ala	Gly	Glu	Ile	Val	Pro	Thr																																							
		35					40					45																																										
Arg	Val	Gln	Asn	Gly	Trp	Arg	Val	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn																																							
	50					55				60																																												
Ser	Leu	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met																																							
	65				70					75					80																																							
Leu	Glu	Arg	Leu	Ala	Gly	Lys	Ser	His	Tyr	Leu	Glu	Arg	Leu	Ala	Gly																																							
				85					90					95																																								
Lys	Ser	His	Tyr	Cys	Cys	Leu	Asp	Gly	Tyr	Glx	Gly	Phe	Phe	Gln	Ile																																							
		100						105					110																																									
Pro	Val	Ala	Pro	Glu	Asp	Gln	Glu	Lys	Thr	Met	Phe	Thr	Cys	Pro	Phe																																							
		115					120						125																																									
Gly	Thr	Phe	Ser	Tyr	Arg	Arg	Met	Pro	Phe	Gly	Leu	Cys	Asn	Ala	Pro																																							
	130					135					140																																											
Ala	Ser	Phe	His	Arg	Cys	Met	Val	Ser	Ile	Phe	Ser	Asp	Tyr	Val	Asp																																							
	145				150					155				160																																								
Lys	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	Thr	Val	Tyr	Gly	Glu	Ser																																							
			165						170				175																																									
Phe	Glu	Val	Ser	Leu	Thr	Asn	Leu	Ala	Lys	Ile	Leu	Glu	Arg	Cys	Leu																																							
		180						185					190																																									
Glu	Phe	Asn	Leu	Val	Leu	Asn	Tyr	Glu	Lys	Cys	His	Phe	Met	Val	Asp																																							
		195					200					205																																										
Lys	Gly	Leu	Val	Leu	Gly	His	Ile	Ile	Ser	Ala	Asp	Gly	Ile	Ser	Val																																							
	210					215					220																																											
Asp	Lys	Ala	Lys	Ile	Asn	Ile	Ile	Asn	Ser	Leu	Pro	Tyr	Pro	Thr	Thr																																							
	225				230				235					240																																								
Val	Arg	Glu	Ile	Trp	Ser	Phe	Leu	Gly	His	Ala	Gly	Phe	Tyr	Lys	Trp																																							
				245					250					255																																								
Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val																																															
		260																																																				

<210> 92

<211> 763

<212> DNA

<213> Gossypium hirsutum

<400> 92

gtgcgtaaaag aggtcgtaaaa gctacttgat tccgggatga tctatcccat atctgacaat 60
aattgggtta gtccagtcca catagtaccc aaaaagaccg gtgtaaccgt aattgagaat 120
tcagcaggtg agatggttcc cacttaagtc cgaaacggtc ggagagtatg catcgattac 180

```

aggaagttga attccttaac tcggaaagat cactttccac ttctttttat tgatcagatg 240
ttagaacatt tagccagaaa gtctcattat tgttgtctgg atggttactc aggttttttc 300
cagatcccaa tggcactaaa ggatcaagaa aagatgacat ttacgtgccc atttggtcatg 360
ttcgcttata gaaggatgtc gtttcagact ttgcaatgca ccaacctgtg ttcagagggtg 420
catgataagt atattttttg actatgttaa gaaaataatt gaggtgttca tggacgaatt 480
tactgtatat agtgagtcct tcgaggtata tttgtcaaat ctagaaaaat ttttggaag 540
atgcttagaa tttaatcttg ttctaaatta tgagaattgc tatttaatgg tagacaagg 600
attagttcta ggtcatatca tttctgctaa gggaatttct gtcgataaag taaaaattaa 660
catcataagc tcaataccat accccacaac tgtgagggag attcgttctt tccttagtca 720
tataggttgc tataggcgtat tcatcaagga cttttcaaaa gtt 763

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<210> 93

<211> 254

<212> PRT

<213> *Gossypium hirsutum*

<400> 93

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Val Arg Lys Glu Val Val Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro
  1              5              10              15

```

```

Ile Ser Asp Asn Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys
          20              25              30

```

```

Thr Gly Val Thr Val Ile Glu Asn Ser Ala Gly Glu Met Val Pro Thr
    35              40              45

```

```

Glx Val Arg Asn Gly Arg Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
    50              55              60

```

```

Ser Leu Thr Arg Lys Asp His Phe Pro Leu Leu Phe Ile Asp Gln Met
    65              70              75              80

```

```

Leu Glu His Leu Ala Arg Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr
          85              90              95

```

```

Ser Gly Phe Phe Gln Ile Pro Met Ala Leu Lys Asp Gln Glu Lys Met
    100              105              110

```

```

Thr Phe Thr Cys Pro Phe Gly Met Phe Ala Tyr Arg Arg Met Ser Phe
    115              120              125

```

```

Arg Leu Cys Asn Ala Pro Thr Met Phe Gln Arg Cys Met Ile Ser Ile
    130              135              140

```

```

Phe Phe Asp Tyr Val Lys Lys Ile Ile Glu Val Phe Met Asp Glu Phe
    145              150              155              160

```

```

Thr Val Tyr Ser Glu Ser Phe Glu Val Tyr Leu Ser Asn Leu Glu Lys
    165              170              175

```

```

Phe Leu Glu Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Asn
    180              185              190

```

```

Cys Tyr Leu Met Val Asp Lys Gly Leu Val Leu Gly His Ile Ile Ser
    195              200              205

```

Ala Lys Gly Ile Ser Val Asp Lys Val Lys Ile Asn Ile Ile Ser Ser
 210 215 220

Ile Pro Tyr Pro Thr Thr Val Arg Glu Ile Arg Ser Phe Leu Ser His
 225 230 235 240

Ile Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 94
 <211> 723
 <212> DNA
 <213> Gossypium hirsutum

<400> 94
 gtgcgtaagg aggttttgaa attgttggat gctggaatga tatactcgat ctttgacagt 60
 gattgggtta gctgggttca tgctgtgcc aagaaaactg gcgtgacagt ggtgaaaaac 120
 tcatcaggag agctagtccc taccgagtc cagaatcgat ggagggtttg catcgattac 180
 aggaagttga acgcagctac ccgaaatgac cattttccac ttcccttcat tgatcaaagt 240
 ctcgagcgat tagctaataa gaccattat tggtgtctcg atgggtactc aggacttttc 300
 caaattccgg tggcacctga ggatcaagac aaaacaactt tcacgtgccc ctttggaacg 360
 tttgcgtata gaagaatgtc gtttgactc tgtaatgctc cggccacttt ccagagatgt 420
 atggtgagca tattctctga ttatgtcgag aaaatcattg aattcttcat ggatgacttc 480
 acggtgtacg gtaactcttt taacgaatgt ctcgataatc ttgctaagat attacagaga 540
 tgcctagaat ttaactctgt tttaaattat gaaaaatgcc acttcatggt tgacaaagga 600
 ttaattttgg gtcatatagt ttcttcagaa ggtattgagg tcaataaagc aaaaacgaat 660
 attattgact cattacctta cccagattt tacagacgat tcataaagga cttcacaaaa 720
 gtt 723

<210> 95
 <211> 241
 <212> PRT
 <213> Gossypium hirsutum

<400> 95
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Gly Met Ile Tyr Ser
 1 5 10 15
 Ile Phe Asp Ser Asp Trp Val Ser Trp Val His Val Val Pro Lys Lys
 20 25 30
 Thr Gly Val Thr Val Val Lys Asn Ser Ser Gly Glu Leu Val Pro Thr
 35 40 45
 Arg Val Gln Asn Arg Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Ala Ala Thr Arg Asn Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn Lys Thr His Tyr Cys Cys Leu Asp Gly Tyr
 85 90 95
 Ser Gly Leu Phe Gln Ile Pro Val Ala Pro Glu Asp Gln Asp Lys Thr
 100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile
 130 135 140

Phe Ser Asp Tyr Val Glu Lys Ile Ile Glu Phe Phe Met Asp Asp Phe
 145 150 155 160

Thr Val Tyr Gly Asn Ser Phe Asn Glu Cys Leu Asp Asn Leu Ala Lys
 165 170 175

Ile Leu Gln Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys
 180 185 190

Cys His Phe Met Val Asp Lys Gly Leu Ile Leu Gly His Ile Val Ser
 195 200 205

Ser Glu Gly Ile Glu Val Asn Lys Ala Lys Thr Asn Ile Ile Asp Ser
 210 215 220

Leu Pro Tyr Pro Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys
 225 230 235 240

Val

<210> 96

<211> 762

<212> DNA

<213> Lycopersicon esculentum

<400> 96

gtgcggaag	agggtgtgaa	gctgttagat	acgggtattg	tctagccaat	ttcggacaac	60
aagtaggtta	gtccagtaca	atgtgaacct	aaaaagggag	acataacggt	gatcactaat	120
gaaaaaaaaatg	agttgatccc	aaccatgata	gtcacataat	ggagaatatg	catggattac	180
aggaaattga	atgaagccac	caggaaggac	cattaccggg	tcccttttat	tgatcagatg	240
ttggaccggt	tggtgggga	ataatattat	tgttttctta	atggctattt	acggtacaac	300
caaattgtga	tttcaccaa	ggattaagag	aaaaccactt	tcacttgccc	gtatggtaca	360
tatgctttca	aaaagatacc	ttttgggtta	tgaaatgcct	cggctacttt	ccaatgatgc	420
atgatggcta	tttttcatga	tatggttgaa	gattttgttg	agatattcat	gaatgatttc	480
tcagtgtttg	gggattcttt	tgatatgtgc	ttggagaatt	tggaacagtgt	gttggctagt	540
tgtgaagaaa	ctaattcttt	cctaaactgg	gaataatagc	aattttctagt	aaaggaaggg	600
attatgctag	gacataaggt	gtcaaagaga	ggatatggaag	ttgatagtgc	caaagtggag	660
gttattgaaa	agcttcccc	tcctatatct	gttaaaggga	tgcaaagttt	tctgggtcat	720
gttgggttct	ataggagatt	cataaaagac	ttcacaaggg	tt		762

<210> 97

<211> 254

<212> PRT

<213> Lycopersicon esculentum

<400> 97

Val Arg Lys Glu Val Val Lys Leu Leu Asp Thr Gly Ile Val Glx Pro

1	5	10	15
Ile Ser Asp Asn Lys Glx Val Ser Pro Val Gln Cys Glu Pro Lys Lys	20	25	30
Gly Asp Ile Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr	35	40	45
Met Ile Val Thr Glx Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn	50	55	60
Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met	65	70	75
Leu Asp Arg Leu Ala Gly Glu Glx Tyr Tyr Cys Phe Leu Asn Gly Tyr	85	90	95
Leu Arg Tyr Asn Gln Ile Val Ile Ser Pro Lys Asp Glx Glu Lys Thr	100	105	110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Lys Ile Pro Phe	115	120	125
Gly Leu Glx Asn Ala Ser Ala Thr Phe Gln Glx Cys Met Met Ala Ile	130	135	140
Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asn Asp Phe	145	150	155
Ser Val Phe Gly Asp Ser Phe Asp Met Cys Leu Glu Asn Leu Asp Ser	165	170	175
Val Leu Ala Ser Cys Glu Glu Thr Asn Leu Phe Leu Asn Trp Glu Glx	180	185	190
Glx Gln Phe Leu Val Lys Glu Gly Ile Met Leu Gly His Lys Val Ser	195	200	205
Lys Arg Gly Met Glu Val Asp Ser Ala Lys Val Glu Val Ile Glu Lys	210	215	220
Leu Pro Pro Pro Ile Ser Val Lys Gly Met Gln Ser Phe Leu Gly His	225	230	235
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val	245	250	

<210> 98

<211> 689

<212> DNA

<213> Lycopersicon esculentum

<400> 98

cgaaggagg tgggtgaaact ggaaattatc aagtagttgg atgctagagt aatctatcca 60
atcgccgata gtagttgggt atgcctagtt cagtgtgtac caaagaaagg gggaatgact 120
gtggtcccca acgaaaagaa tgaacttggt cgaatgagac cggttactgg atggagggtg 180

tgcacggatt accgtaaact gaactcatag actgaaaaag actatitttca tatgcccttc 240
 atggatcaga tggttgatag acttgccgga aaaggggtgt attgttttct tgatgggtat 300
 tcgggggtata atcagatttc tattgcacca gaagatcaag agaaaaccac tttcacttgt 360
 ccatacggga cttttgcatt cagaagaatg tcgtttgggt tgtgcaatgc acccgcaacc 420
 tttcagagat ggatgatgtc aatattttct gacatgatgg aggatactat agaggttttt 480
 atggatgatt tttctgtggt tggtgattca ttcgagcggg gcttgtccaa tttatctgag 540
 gttcttaaga gatgtgaaga ctgcaatttg gtactaaact gggaaaagtg tcatttcatg 600
 gtgaaagagg gtattgtgtt gggcatcgc atttcagaaa agggcatgca tgtttttact 660
 ggtgattcat caaagacttc acaaagggt 689

<210> 99

<211> 229

<212> PRT

<213> *Lycopersicon esculentum*

<400> 99

Arg Lys Glu Val Val Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala Arg
 1 5 10 15

Val Ile Tyr Pro Ile Ala Asp Ser Ser Trp Val Cys Leu Val Gln Cys
 20 25 30

Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Glu Lys Asn Glu
 35 40 45

Leu Val Arg Met Arg Pro Val Thr Gly Trp Arg Val Cys Met Asp Tyr
 50 55 60

Arg Lys Leu Asn Ser Glx Thr Glu Lys Asp Tyr Phe His Met Pro Phe
 65 70 75 80

Met Asp Gln Met Leu Asp Arg Leu Ala Gly Lys Gly Trp Tyr Cys Phe
 85 90 95

Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ser Ile Ala Pro Glu Asp
 100 105 110

Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Arg
 115 120 125

Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Trp
 130 135 140

Met Met Ser Ile Phe Ser Asp Met Met Glu Asp Thr Ile Glu Val Phe
 145 150 155 160

Met Asp Asp Phe Ser Val Val Gly Asp Ser Phe Glu Arg Cys Leu Ser
 165 170 175

Asn Leu Ser Glu Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu
 180 185 190

Asn Trp Glu Lys Cys His Phe Met Val Lys Glu Gly Ile Val Leu Gly
 195 200 205

His Arg Ile Ser Glu Lys Gly Met His Val Phe Thr Gly Asp Ser Ser

210

215

220

Lys Thr Ser Gln Arg
225

<210> 100

<211> 760

<212> DNA

<213> Lycopersicon esculentum

<400> 100

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gtgCGtaagg aggtgtttaa gcttctagat gCGggtattg tctacccaat taggacaaca 60
agtgggtag tctagtacaa tgtgtaccta aaaagggagg catggcaatg attactaatg 120
aaaacaatga gtttatccca accagcacag tcacaagatg gcgaatatgc atgaattaca 180
cgaagttaat gaagccacta ggaagaatca ttaccaatt ctttttattg attatatgtt 240
ggaccgggta gctgggcaag aatattattg ttttttggat tactaatcag ggtacaacta 300
aattttgatt gcaccagagg atcaagagaa aacaactttc acttgcccgat atggtacata 360
tgctttcaag aggatacctt ttgggttatg caatgctctg tctaatttcc aaagatgcat 420
gatgactatt tttcatgata tgggtgaata ttttgaggat atattcatgg atgatttctt 480
agtgttttgg gagtcttttg atagatgctt ggagaatttg aacagggttg tagctagggtg 540
cgaacaaact aatcttgtcc tgaactggga aaaatgtcat ttttagtaa aggaagggaa 600
tttttcgggg cataaggtgt aaaagatagg gctggaagtt gatcatgaca aagtggaggt 660
aattgaaaag atctctcttc ccatttttgt gaaacgggtg agaagtttac taggtcatgc 720
tgagttttac aggatattca tcaaggactt ctcaaagggt 760

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<210> 101

<211> 254

<212> PRT

<213> Lycopersicon esculentum

<400> 101

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Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
 1           5           10           15

Ile Ser Asp Asn Lys Trp Val Ser Leu Val Gln Cys Val Pro Lys Lys
      20           25           30

Gly Gly Met Ala Met Ile Thr Asn Glu Asn Asn Glu Phe Ile Pro Thr
      35           40           45

Ser Thr Val Thr Arg Trp Arg Ile Cys Met Asn Tyr Thr Lys Leu Asn
      50           55           60

Glu Ala Thr Arg Lys Asn His Tyr Pro Ile Leu Phe Ile Asp Tyr Met
      65           70           75           80

Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Tyr Glx
      85           90           95

Ser Gly Tyr Asn Glx Ile Leu Ile Ala Pro Glu Asp Gln Glu Lys Thr
      100          105          110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Ile Pro Phe
      115          120          125

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Gly Leu Cys Asn Ala Leu Ser Asn Phe Gln Arg Cys Met Met Thr Ile
 130 135 140

Phe His Asp Met Val Glu Tyr Phe Glu Asp Ile Phe Met Asp Asp Phe
 145 150 155 160

Leu Val Phe Trp Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asn Arg
 165 170 175

Leu Leu Ala Arg Cys Glu Gln Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Leu Val Lys Glu Gly Asn Phe Ser Gly His Lys Val Glx
 195 200 205

Lys Ile Gly Leu Glu Val Asp His Asp Lys Val Glu Val Ile Glu Lys
 210 215 220

Ile Ser Ser Pro Ile Phe Val Lys Arg Val Arg Ser Leu Leu Gly His
 225 230 235 240

Ala Glu Phe Tyr Arg Ile Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 102
 <211> 776
 <212> DNA
 <213> Lycopersicon esculentum

<400> 102
 gtgcggaag aagtgtttaa actggaatca ttaaattggtt ggatgctgga gtaatatac 60
 cgatctccga tagtagttgg gtatgcccta ttcagtgtgt acctaagaaa gggggaatga 120
 ctgtggtccc caataagaaa aatgaacttg ttctaattgag accggttact ggagggtggg 180
 tgtgtatgga ttaccgtaaa ttaaattgcat ggactgaaaa agaccatttt cctatgccct 240
 tcatggatca gatgttggat agacttgccg aaaaagggtg gtactgtttt cttgatggat 300
 agtcagggtg taattagatt tctattgcac cagaagatca agagaaaacc acatttactt 360
 gtccatatgg gacctttgca ttgaagagaa tgtcgtttgg gttgtgcaat gcaccgcca 420
 catttcacag atgtaaaaat gttgatattc ttcgacatgg tggatgatac tattgatgct 480
 tttatggatg atttttctct tgttgggtgaa tcattcgaga ggtgtttgaa ccatttatct 540
 gatgtcctta agagatgtga agactgcaat ttagtactaa attgggaaaa atgccacttc 600
 atggtgaaaa aaggtattgt tttgggtcat cgcattccag aaaagggtcat agaggttgat 660
 cgagctaaag tagaggtaat agagagactt cccccactat ctctgtaaaa ggtgtgagaa 720
 gctttcttgg gcatgcaagt ttttaccgga gattcatcaa agacttcaca aaagtt 776

<210> 103
 <211> 258
 <212> PRT
 <213> Lycopersicon esculentum

<400> 103
 Ala Glu Arg Ser Val Glx Thr Gly Ile Ile Lys Trp Leu Asp Ala Gly
 1 5 10 15
 Val Ile Tyr Pro Ile Ser Asp Ser Ser Trp Val Cys Pro Ile Gln Cys
 20 25 30

Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Lys Lys Asn Glu
 35 40 45
 Leu Val Leu Met Arg Pro Val Thr Gly Gly Trp Val Cys Met Asp Tyr
 50 55 60
 Arg Lys Leu Asn Ala Trp Thr Glu Lys Asp His Phe Pro Met Pro Phe
 65 70 75 80
 Met Asp Gln Met Leu Asp Arg Leu Ala Glu Lys Gly Trp Tyr Cys Phe
 85 90 95
 Leu Asp Gly Glx Ser Gly Tyr Asn Glx Ile Ser Ile Ala Pro Glu Asp
 100 105 110
 Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Leu Lys
 115 120 125
 Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe His Arg Cys
 130 135 140
 Lys Met Leu Ile Phe Phe Asp Met Val Asp Asp Thr Ile Asp Ala Phe
 145 150 155 160
 Met Asp Asp Phe Ser Leu Val Gly Glu Ser Phe Glu Arg Cys Leu Asn
 165 170 175
 His Leu Ser Asp Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu
 180 185 190
 Asn Trp Glu Lys Cys His Phe Met Val Lys Lys Gly Ile Val Leu Gly
 195 200 205
 His Arg Ile Pro Glu Lys Gly Ile Glu Val Asp Arg Ala Lys Val Glu
 210 215 220
 Val Ile Glu Arg Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser
 225 230 235 240
 Phe Leu Gly His Ala Ser Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr
 245 250 255
 Lys Val

<210> 104
 <211> 761
 <212> DNA
 <213> Solanum tuberosum

<400> 104
 gtgcggaagg aggtacttaa attgttgat gcacggattg tgtacccaat atcagacagt 60
 aaatgggtaa gtccagtaaa gtgtgtgccc aagaaggga gaatgacggt gttgactaat 120
 gagaagaatg aggtaatccc cacaagaaca gtgactgggt gacggatttg catggactac 180
 atgaagttga acgacgccac cagaaaggac cattatccg tacctttcat tgataaaata 240

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ttggataggt tggcaggaca tgagtactat tgttttcttg gtgtctactc aggggtacaat 300
cagattgtta ttgcaataga ggactaggtg aaaaccacct tcacctgttc gtatggcaca 360
tatgcgttca agcacatgcc attcggcttg tgcaatgccc tggccacatt tcagagatgc 420
atgttggcaa tcttccatga tatggtggag gattttgttg aagttttcat ggatgacttc 480
ttggtgtttg gtgagtcctt tgaactttgt ttgactaatt ttgacagatt tcttgctagg 540
tgtgaagaga cgaatctggt gataaactga tagaagtgtc actttctggt tcgagaggga 600
attgtgttgg gacacaagat ctccaaaaat gggctgaaag ttgacaaagc caacgtagag 660
gttattgaga aattgccacc cccatcacag tgaaggtaat taaaagctta ctaggacatg 720
cttggtttta tacgaggttc atcaaagact tcacaaaggt t 761

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<210> 105
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 105
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Arg Ile Val Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Lys Trp Val Ser Pro Val Lys Cys Val Pro Lys Lys
 20 25 30
 Gly Arg Met Thr Val Leu Thr Asn Glu Lys Asn Glu Val Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Glx Arg Ile Cys Met Asp Tyr Met Lys Leu Asn
 50 55 60
 Asp Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Lys Ile
 65 70 75 80
 Leu Asp Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Gly Val Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Ile Glu Asp Glx Val Lys Thr
 100 105 110
 Thr Phe Thr Cys Ser Tyr Gly Thr Tyr Ala Phe Lys His Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Leu Ala Thr Phe Gln Arg Cys Met Leu Ala Ile
 130 135 140
 Phe His Asp Met Val Glu Asp Phe Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Leu Val Phe Gly Glu Ser Phe Glu Leu Cys Leu Thr Asn Phe Asp Arg
 165 170 175
 Phe Leu Ala Arg Cys Glu Glu Thr Asn Leu Val Ile Asn Glx Glx Lys
 180 185 190
 Cys His Phe Leu Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Lys Asn Gly Leu Lys Val Asp Lys Ala Asn Val Glu Val Ile Glu Lys

210 215 220
 Leu Pro Pro Pro Ile Thr Val Lys Val Ile Lys Ser Leu Leu Gly His
 225 230 235 240

Ala Trp Phe Tyr Thr Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 106
 <211> 760
 <212> DNA
 <213> Solanum tuberosum

<400> 106
 gtgcgtaaag aggttttcaa actgctagat gtcggtattg tatatccgat ttcagaaaagc 60
 aaatgggtca gccagtttta gtgtgtgcct aaaaaaagag gcatgccggt gatcaccaat 120
 gaaaaaaatg agttgattcc aaccaggaca gtgacagggt gccgaatatg catggattat 180
 aggaaattga atgaggccac cagaaaggat cactgcccgg ttccttttat tgatcagatg 240
 ctggacagggt tagttgggca agaattattat tgtttcctgg aaggctattc aggatacaac 300
 caaattgtga ttgcaccaga ggaccaggag aaaactacat tcacttgtct gtatgggaca 360
 tatgctttca agtgactgcc gtttgggcta tgcaatgctc cagccacctt ccaaagatga 420
 atgatggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc 480
 tcagtcttta gggagtcttt tgataggtgt ttggagaatt gggacagggt gctggctaga 540
 tgcgaggaaa ctaatctcat cctaaactgg aaaaaatgtc atttcctagt aaatgaaggg 600
 attgtattgg gccataaggt gtcaaagaga gggctggaag ttgatcgtgc caaagtggaa 660
 gttattgaaa aactacctcc tccaatctgt taaaggggtg agaagctttc tgggtcatgc 720
 tggtttttac aggagattta taaaggactt cacaaagggt 760

<210> 107
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 107
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Ser Glu Ser Lys Trp Val Ser Pro Val Glx Cys Val Pro Lys Lys
 20 25 30
 Arg Gly Met Pro Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Cys Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Val Gly Gln Glu Tyr Tyr Cys Phe Leu Glu Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Glu Lys Thr
 100 105 110

Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Ala Phe Lys Glx Leu Pro Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Glx Met Met Ala Ile
 130 135 140

Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe
 145 150 155 160

Ser Val Phe Arg Glu Ser Phe Asp Arg Cys Leu Glu Asn Trp Asp Arg
 165 170 175

Val Leu Ala Arg Cys Glu Glu Thr Asn Leu Ile Leu Asn Trp Lys Lys
 180 185 190

Cys His Phe Leu Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205

Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 108
 <211> 761
 <212> DNA
 <213> Solanum tuberosum

<400> 108
 gtgcgtaaag aggttttcaa gctctggatg caggtattgt ctatccaatt tcagacagca 60
 agtgggtcag tccagttcag tgtgtgccta aaaagggagg catgacgggtg atcactaatg 120
 aaaaaaatga gttgattcca accaggacag tgacaggatg gcgaatatgc atggattaca 180
 gaaaattaaa tgaagctacc agaaaggatc actaccgggt tccttttatt gatcagatgc 240
 tggacagggtt ggctggacaa gaatattatt gtttcttgga tggttattca ggatacaacc 300
 aaatagtgat tgcaccagag gaccagggga aaactacatt cacttgcttg tatgggacat 360
 atgtttccaa gagaatgtcg tttgggctat gcaatgctcc atccattttc caaagatgca 420
 tgatggccat cttccatgat aaggttgaag attttatgga aatattcatg gatgacttct 480
 cagtatttgg ggagtccttt gacagggtgct tggagaattt agacagagtg ttggctagat 540
 gcgaggaaac taattttgtc ctaaactggg aaaaatgtca tttcctagtg aaggaagggg 600
 ttgtgttggg tcataaggtg tcaaagagag ggctggaagt tgatcgtgcc agagtggaaa 660
 taatcaaaaa gctacctccc ccaatttctg ttaaaggggt gcgaagtttt ttgggtcatg 720
 ttagtttcta cgaaagattc ataaaggact tcaccaaggt t 761

<210> 109
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 109
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15

Ile Ser Asp Ser Lys Trp Val Ser Pro Val Gln Cys Val Pro Lys Lys
 20 25 30

Gly Gly Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45

Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60

Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80

Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95

Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Gly Lys Thr
 100 105 110

Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Val Ser Lys Arg Met Ser Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Ser Ile Phe Gln Arg Cys Met Met Ala Ile
 130 135 140

Phe His Asp Lys Val Glu Asp Phe Met Glu Ile Phe Met Asp Asp Phe
 145 150 155 160

Ser Val Phe Gly Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asp Arg
 165 170 175

Val Leu Ala Arg Cys Glu Glu Thr Asn Phe Val Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205

Lys Arg Gly Leu Glu Val Asp Arg Ala Arg Val Glu Ile Ile Lys Lys
 210 215 220

Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240

Val Ser Phe Tyr Glu Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 110

<211> 762

<212> DNA

<213> Solanum tuberosum

<400> 110

gtgcgtaagg aggtcctcaa gctgtctgat gcaggaattg tgtaccccat ttatgatata 60
 aagtggatca gccagttca ctgtgtgccg aaaaaggag gcatgacgat tattactaat 120
 gaaaagaagg agttgatttc agctagaacg gtgatagagt ggcacatatg aatggactat 180
 aggagactaa atgaggcaac tagaaaggaa cactaccag ttcctttcat tgatcaaatg 240

ttggacaggt ttattgggca agagtattat tgtttcctag atggctattc aggatataat 300
 caaattgtga ttgcgccata agataaagag aaaactacat ttacttctct atatgggaca 360
 tatgccttca agagaatgtc gtttgggccc tgcaatgtc caaccacatt ccaaagatgc 420
 atgacagcca tttttcatga tatgggtcaaa tattttgtgg agatattcat ggatgaattc 480
 ttagtccttg gggagtcctt tgacacgtgt ctagaatatt tggacaatgt gcttgccaga 540
 tgtgaggaaa ctaatcccgt cctcaactgg gaaaaatgtc attttctagt gaagaagggg 600
 attgtactag gccacaaggt ttcagaggaa ggactggaag ttgatcgtgg aaaagtagag 660
 gtaatttaaa agctaccccc tcaagtcttc gttaaagggg tgagaagggt ccttggtcat 720
 tctaggttcg aaatgagatt cataaaagac ttcacaaaag tt 762

<210> 111
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 111
 Val Arg Lys Glu Val Leu Lys Leu Ser Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Tyr Asp Ile Lys Trp Ile Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Ile Ile Thr Asn Glu Lys Lys Glu Leu Ile Ser Ala
 35 40 45
 Arg Thr Val Ile Glu Trp His Ile Glx Met Asp Tyr Arg Arg Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Glu His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Phe Ile Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glx Asp Lys Glu Lys Thr
 100 105 110
 Thr Phe Thr Ser Leu Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
 115 120 125
 Gly Pro Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Thr Ala Ile
 130 135 140
 Phe His Asp Met Val Lys Tyr Phe Val Glu Ile Phe Met Asp Glu Phe
 145 150 155 160
 Leu Val Phe Gly Glu Ser Phe Asp Thr Cys Leu Glu Tyr Leu Asp Asn
 165 170 175
 Val Leu Ala Arg Cys Glu Glu Thr Asn Pro Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Lys Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Glu Gly Leu Glu Val Asp Arg Gly Lys Val Glu Val Ile Glx Lys

210 215 220
 Leu Pro Pro Gln Val Phe Val Lys Gly Val Arg Arg Phe Leu Gly His
 225 230 235 240
 Ser Arg Phe Glu Met Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 112
 <211> 762
 <212> DNA
 <213> Solanum tuberosum

<400> 112
 gtgcggaagg aggttttttaa gctgctggat gcgggtattg tataccagat ttcagatagc 60
 aaaggggtct acccgattta gtttgtgcct aaaaaatgca gcatgacagt gatcaccaat 120
 gaaaagaatg agctgattcc aaccaggaca gtgacagggt ggcgaatatg catggattat 180
 atgaagttga atgaggccac cagaaaggat cactacccga ttcattttat tgatcagatg 240
 ttggacaagt tagctgagta aaaatattat tgtttcttgg cttgttattc aagatacaac 300
 caattttctca ttgcaccaca ggaccaggag gaaactacat tcacttgtcc ttatgggaca 360
 tatgcttttca agcgaatgtc gtttgggcta tgcaatgctc caaccacctt ccaaagatgc 420
 ataagggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc 480
 tcagtctttg ggtagtcttt tgagaggtgt ctggaaaatt ttgacagggt gctggctgta 540
 tgcgaggaaa ctaatttttt cctaaactgg gaaaaatgct attttctagt gaaggaaggg 600
 attgtattgg gacataaggt gtcaaagtga aggcttgaag ttgatcgtgc caaagtggaa 660
 gtcgttgaaa acctaccttc cccattctct gttaaagggt tgagaagttt tttgggtcat 720
 gctggtttct ataggagatt tatcaaagac ttcactaagg tt 762

<210> 113
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 113
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Gln
 1 5 10 15
 Ile Ser Asp Ser Lys Gly Val Tyr Pro Ile Glx Phe Val Pro Lys Lys
 20 25 30
 Cys Ser Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Met Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Tyr Pro Ile His Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Lys Leu Ala Glu Glx Lys Tyr Tyr Cys Phe Leu Ala Cys Tyr
 85 90 95
 Ser Arg Tyr Asn Gln Phe Leu Ile Ala Pro Gln Asp Gln Glu Glu Thr
 100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Ile Arg Ala Ile
 130 135 140

Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe
 145 150 155 160

Ser Val Phe Gly Glx Ser Phe Glu Arg Cys Leu Glu Asn Phe Asp Arg
 165 170 175

Val Leu Ala Val Cys Glu Glu Thr Asn Phe Phe Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205

Lys Glx Arg Leu Glu Val Asp Arg Ala Lys Val Glu Val Val Glu Asn
 210 215 220

Leu Pro Ser Pro Phe Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 114
 <211> 793
 <212> DNA
 <213> Solanum tuberosum

<400> 114
 aacttttgtg aagtcttta tgaaggatgt tgtcagagaa gaagtcatca agtggctgga 60
 tacagggatt gtgtacccaa tatctgacaa taaatgggca agtccagtgc agtgtgtgcc 120
 taaaaaggga ggaatgacag ttgtgaccaa tgagaaaaat gagttgatcc ccacaagaac 180
 agtaactggg tggaggctat gcatggacta cagaaaactc aatgaagcca ccaggaagga 240
 ccactattcg gtaccgttca ttgatcaaat gttagacagg ttggctggcc aagagtatta 300
 ctgtttcctt gatggttatt caaggataaa ttagatcgtc attgcacctg aggatcaaga 360
 gaatacgaca ttcacttgcc catatggcac gtatgcattc aaacgcttgc cattcggctt 420
 gtgcaatgcc ccaaccctat ttcagagatg tatgatggca atcttccatg atatggtgga 480
 agattttgtt aaagtataca tggacgattt ctcggtgttt ggtgagtcgt tcgaactttg 540
 tttatctaata cgtgatagag ttcttactag gtgtgaggag accaatttgg tgctgaactg 600
 ggagaagtgt cactttcttg tcagagaagg aattatgttg gggcagaaga tctccaaaag 660
 tgggctagaa gtagacaagg cgaaggtgga agtgattgag aagttgccac caccaatata 720
 agtaaaggga gtgcgaagct tccttgga tgcgtgtttt tacaagaggt tcataaagga 780
 cttttcaaag gtt 793

<210> 115
 <211> 264
 <212> PRT
 <213> Solanum tuberosum

<400> 115
 Thr Phe Val Lys Ser Leu Met Lys Asp Val Val Arg Glu Glu Val Ile

1	5	10	15
Lys Trp Leu Asp Thr Gly Ile Val Tyr Pro Ile Ser Asp Asn Lys Trp	20	25	30
Ala Ser Pro Val Gln Cys Val Pro Lys Lys Gly Gly Met Thr Val Val	35	40	45
Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr Arg Thr Val Thr Gly Trp	50	55	60
Arg Leu Cys Met Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp	65	70	75
His Tyr Ser Val Pro Phe Ile Asp Gln Met Leu Asp Arg Leu Ala Gly	85	90	95
Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Arg Tyr Asn Glx Ile	100	105	110
Val Ile Ala Pro Glu Asp Gln Glu Asn Thr Thr Phe Thr Cys Pro Tyr	115	120	125
Gly Thr Tyr Ala Phe Lys Arg Leu Pro Phe Gly Leu Cys Asn Ala Pro	130	135	140
Thr Leu Phe Gln Arg Cys Met Met Ala Ile Phe His Asp Met Val Glu	145	150	155
Asp Phe Val Lys Val Tyr Met Asp Asp Phe Ser Val Phe Gly Glu Ser	165	170	175
Phe Glu Leu Cys Leu Ser Asn Arg Asp Arg Val Leu Thr Arg Cys Glu	180	185	190
Glu Thr Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Leu Val Arg	195	200	205
Glu Gly Ile Met Leu Gly Gln Lys Ile Ser Lys Ser Gly Leu Glu Val	210	215	220
Asp Lys Ala Lys Val Glu Val Ile Glu Lys Leu Pro Pro Pro Ile Glx	225	230	235
Val Lys Gly Val Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Lys Arg	245	250	255
Phe Ile Lys Asp Phe Ser Lys Val	260		

<210> 116

<211> 761

<212> DNA

<213> Platanus occidentalis

<400> 116

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gtgCGtaagg aggttttcaa acttcttaaa gtttgagtga tttatcctat ttaggatagg 60
aattgggtca gcccggttca agtggttcct aaaaagattg gaataaccgt tgtgaaaaat 120
tagaatgatg agttggttcc taccagtgtt cagaatgggt ggagggttgt atagattata 180
gaaaattgaa tgttgaacc cgcaaggatc acttcccttt accctttatt gatcaaatgc 240
ttgaaaggtt agttggtcat tcttactatt gtttcctaga tggttattca agttatttcc 300
agattgtaat tactccagag gattaagaaa agacaacttt tacatgtcca tttgggactt 360
ttgcatatcg ttgcatgccc tttggccttt gcaatgcccc aaccactttc caaagggtga 420
tggttagcat attttcatat tacattgaga atatcataga agtttttatg gatgatttca 480
tagtttatgg agactccttt aataattttc tgcataacct tacacttggt cttcaaagat 540
gcatagaaac taacctgtg ttaaattatg aaaaatgtca ttttatgggt gaacaaggta 600
tagttttggg tcatgttatt tcatctaaag gaattgaggt agataaagct aaagttgata 660
ttattcaatc tttaccttat ctcatagta tgcggaaagt tcattctttt cttggacatg 720
caggtttcta ccgaagattc attaaagact ttacaaaggt t 761

```

<210> 117

<211> 254

<212> PRT

<213> *Platanus occidentalis*

<400> 117

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Val Arg Lys Glu Val Phe Lys Leu Leu Lys Val Glx Val Ile Tyr Pro
  1             5             10             15

```

```

Ile Glx Asp Arg Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
      20             25             30

```

```

Ile Gly Ile Thr Val Val Lys Asn Glx Asn Asp Glu Leu Val Pro Thr
      35             40             45

```

```

Ser Val Gln Asn Gly Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
      50             55             60

```

```

Val Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
      65             70             75             80

```

```

Leu Glu Arg Leu Val Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
      85             90             95

```

```

Ser Ser Tyr Phe Gln Ile Val Ile Thr Pro Glu Asp Glx Glu Lys Thr
      100            105            110

```

```

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe
      115            120            125

```

```

Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Val Ser Ile
      130            135            140

```

```

Phe Ser Tyr Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe
      145            150            155            160

```

```

Ile Val Tyr Gly Asp Ser Phe Asn Asn Phe Leu His Asn Leu Thr Leu
      165            170            175

```

```

Val Leu Gln Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Tyr Glu Lys
      180            185            190

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Cys His Phe Met Val Glu Gln Gly Ile Val Leu Gly His Val Ile Ser
 195 200 205

Ser Lys Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ile Ile Gln Ser
 210 215 220

Leu Pro Tyr Leu Ile Ser Met Arg Lys Val His Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 118
 <211> 762
 <212> DNA
 <213> Platanus occidentalis

<400> 118
 gtgcgtaagg aagttttcaa gcttcttgaa gttggagtga tttatcttat ttcgaatagc 60
 aattgggtta gccagttca agtggctcct aaaaagactg gaataaccgt tgtgaaaaat 120
 cagaatgatg agttagttcc tacccatggt cagaatgggt ggtgggtttg tataaattat 180
 agaaaattaa atgttataac ctgcaaggat cacttccctt taccttttat tgataaaatg 240
 cttgaaagggt tagctgggtca ttcttactat tgtttccttg atggttattt aggttatttt 300
 caaattgcaa ttacttcgga ggatcaagaa aagatgattt ttaagtgcc attcgggact 360
 tttgcataac gtcacatgcc ctttggcctt tgcaatgccc caaccacttt ctaaagggtgt 420
 atggttagca tattttcaga ttacattgag aatatcatag aagtctttat ggatgatttc 480
 acagtttatg gagactcctt tgataattgt ctgcataacc ttacacttgt tattcaaaga 540
 tgcatagaaa ctaacctagt gttaaattct taaaaatgtc attttatggt tgaacaagg 600
 atagttttgg gtcattgttg ttcatctagg ggaattgagg tagataaacc taaagttgat 660
 attattcaaa ctttacctta ttccactagt gtgcgagaag ttcgttcttt tcttggacat 720
 gtagggtttt actgaagatt cataaaagac ttcacaaagg tt 762

<210> 119
 <211> 254
 <212> PRT
 <213> Platanus occidentalis

<400> 119
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Val Gly Val Ile Tyr Leu
 1 5 10 15
 Ile Ser Asn Ser Asn Trp Val Ser Pro Val Gln Val Ala Pro Lys Lys
 20 25 30
 Thr Gly Ile Thr Val Val Lys Asn Gln Asn Asp Glu Leu Val Pro Thr
 35 40 45
 His Val Gln Asn Gly Trp Trp Val Cys Ile Asn Tyr Arg Lys Leu Asn
 50 55 60
 Val Ile Thr Cys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Lys Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95

Leu Gly Tyr Phe Gln Ile Ala Ile Thr Ser Glu Asp Gln Glu Lys Met
 100 105 110

Ile Phe Lys Cys Pro Phe Gly Thr Phe Ala Tyr Arg His Met Pro Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Cys Met Val Ser Ile
 130 135 140

Phe Ser Asp Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160

Thr Val Tyr Gly Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu
 165 170 175

Val Ile Gln Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Ser Glx Lys
 180 185 190

Cys His Phe Met Val Glu Gln Gly Ile Val Leu Gly His Val Val Ser
 195 200 205

Ser Arg Gly Ile Glu Val Asp Lys Pro Lys Val Asp Ile Ile Gln Thr
 210 215 220

Leu Pro Tyr Ser Thr Ser Val Arg Glu Val Arg Ser Phe Leu Gly His
 225 230 235 240

Val Gly Phe Tyr Glx Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 120
 <211> 759
 <212> DNA
 <213> Platanus occidentalis

<400> 120
 gtgcggaag aggttttta gcttttggat gtagggatta tatacccaat tttttatagt 60
 aattaggttaa gtcccaactca agtggaccca agaattctgg tgtgactgta gttaaaaatg 120
 caaatgatga attgattcca aatagactca ctattgggtg gcgtgtatgc attaactata 180
 agaagttgaa ctcagtgact aggaaggacc atttcccttt accattcatg actaaatcct 240
 agaaagggtg gctgggcaca aattttatta tttcctatat gggttattcta gatataacta 300
 aatagagatt gcacctgagg actaagaaaa taccactttt acatgtccat ttggcacttt 360
 tgcttatcga aggatgtcat ttggattatg taatgctctt gccacgttct aaagatgcat 420
 gttgagtata tttagtata tggtagaaca ttttcttgag gtgtttatgg attttttttg 480
 tttttggtaa ttcatttgat gattgtttgc ataatttgaa aaaagtgtta aatagatgtg 540
 aaggaaaaaa acatcatttt gaattgagag aagtgtcatt tcatgggtctc taaaagaatt 600
 gtacttggtc acattgtctc ctccaagga attaaagtgg tcaaagccaa aattgaattg 660
 atagtcaatt tgcctagccc aaagactctt aaagacattc gatcttttct aggtcatgca 720
 ggatttaaca aaaggttcat caaagacttc acgaaaagtt 759

<210> 121
 <211> 254
 <212> PRT
 <213> Platanus occidentalis

<400> 121

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro
1 5 10 15

Ile Phe Tyr Ser Asn Glx Val Ser Pro Thr Gln Val Val Pro Lys Asn
20 25 30

Ser Gly Val Thr Val Val Lys Asn Ala Asn Asp Glu Leu Ile Pro Asn
35 40 45

Arg Leu Thr Ile Gly Trp Arg Val Cys Ile Asn Tyr Lys Lys Leu Asn
50 55 60

Ser Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Glx Ile
65 70 75 80

Leu Glu Arg Val Ala Gly His Lys Phe Tyr Tyr Phe Leu Tyr Gly Tyr
85 90 95

Ser Arg Tyr Asn Glx Ile Glu Ile Ala Pro Glu Asp Glx Glu Asn Thr
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe
115 120 125

Gly Leu Cys Asn Ala Leu Ala Thr Phe Glx Arg Cys Met Leu Ser Ile
130 135 140

Phe Ser Asp Met Val Glu His Phe Leu Glu Val Phe Met Asp Asp Phe
145 150 155 160

Phe Val Phe Gly Asn Ser Phe Asp Asp Cys Leu His Asn Leu Lys Lys
165 170 175

Val Leu Asn Arg Cys Glu Glu Lys Asn Ile Ile Leu Asn Glx Glu Lys
180 185 190

Cys His Phe Met Val Ser Lys Arg Ile Val Leu Gly His Ile Val Ser
195 200 205

Ser Gln Gly Ile Lys Val Val Lys Ala Lys Ile Glu Leu Ile Val Asn
210 215 220

Leu Pro Ser Pro Lys Thr Leu Lys Asp Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Asn Lys Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 122

<211> 761

<212> DNA

<213> Platanus occidentalis

<400> 122

tgcgtaaaga ggtgggtcaag cttcttgaag ttggagtgat ttatcctatt tcggatagca 60
 attggggttag cccgggttcaa gtgggttccta aaaagactgg aataaccgtt gtgaaaaatc 120
 aaaatgatga gttagttcct acccgtgttc agaatgggtg gcaggtttgt atagattata 180
 taaaattaaa tggtgtaacc cgcaaggatc acttcccttt accttttatt gatcaaatgt 240
 ttgaaagggt agctgggtcat tcttactatt gtttccttga tggatattca tggtattttt 300
 agattgcaat tactccagag gatcaagaaa agacgacttt tacgtgcccc ttcgggactt 360
 tttcatatcg ttgcatgccc tttggccttt gcaacgcccc agccactttc caaagggtga 420
 tggtttagcat attttcagat tacattgaga atatcataga agtctttatg gatgatttca 480
 tagtttatga agactccttt gataattgtc tgcataacct tacacttggt ttttaaagat 540
 gcatagaaac taaccttggtg ttaaattttg aaaaatgtca tgttatgggt gaataaggta 600
 tagttttggg tcatgttggt tcatctatgg gaattgaggt agataaagtt aaagttgata 660
 ttattcaatc tttaccttat cccattagtg tgcaggaagt tcgttctttt cttggacatg 720
 cgggttttta ccaaagattc attaaagact tcacgaaagt t 761

<210> 123

<211> 253

<212> PRT

<213> Platanus occidentalis

<400> 123

Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Val Ile Tyr Pro Ile
 1 5 10 15

Ser Asp Ser Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Thr
 20 25 30

Gly Ile Thr Val Val Lys Asn Gln Asn Asp Glu Leu Val Pro Thr Arg
 35 40 45

Val Gln Asn Gly Trp Gln Val Cys Ile Asp Tyr Ile Lys Leu Asn Val
 50 55 60

Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met Phe
 65 70 75 80

Glu Arg Leu Ala Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser
 85 90 95

Cys Tyr Phe Glx Ile Ala Ile Thr Pro Glu Asp Gln Glu Lys Thr Thr
 100 105 110

Phe Thr Cys Pro Phe Gly Thr Phe Ser Tyr Arg Cys Met Pro Phe Gly
 115 120 125

Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile Phe
 130 135 140

Ser Asp Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe Ile
 145 150 155 160

Val Tyr Glu Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu Val
 165 170 175

Phe Glx Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Phe Glu Lys Cys
 180 185 190

His Val Met Val Glu Glx Gly Ile Val Leu Gly His Val Val Ser Ser
 195 200 205

Met Gly Ile Glu Val Asp Lys Val Lys Val Asp Ile Ile Gln Ser Leu
 210 215 220

Pro Tyr Pro Ile Ser Val Gln Glu Val Arg Ser Phe Leu Gly His Ala
 225 230 235 240

Gly Phe Tyr Gln Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 124
 <211> 761
 <212> DNA
 <213> Sorghum bicolor

<400> 124
 gtgcgtaaag aggtcttcaa gctctatcat gctgggatta tttatcctgt gccgcatagt 60
 gagtggggta gccctgttca agtagtgcca aagaaaggag gaatgacggt cgtaggaat 120
 gagaagaatg aactcatccc tcaacgaatt gtcactgggt ggcgtatgtg tattgactat 180
 caaaaactca acacggctac aaagaaagat aactttccgt tacccttcat tgatgaaatg 240
 ttggaacggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac 300
 caaatcccaa tccaccaga tgaccaagaa aagactacct ttacatgccc gtatggaact 360
 tatgcataac gacgaatgac gttcggactg tgcaatgctc cagcttcttt ccaacggtgc 420
 atgatgtcta ttttctcgga catgattgag aagatcatgg aggttttcat ggatgatatt 480
 accgtctatg gtaaaacctt cgatcattgt ttggagaatt tagatagagt cttgcagcga 540
 tgtgaagaaa agcaacttaat cctgaactgg gagaaatgcc attttatggt tcaggaagga 600
 atagtgctag gacataaagt gtccgaacgt ggtatagagg tggacaaagc aaagattgaa 660
 gttattgaaa aacttccacc tcccacgaat gtgaaaggat ccgtagcttc ttgggacatg 720
 cagggttcta tagatgcttc ataaaagact tcacaaagg t 761

<210> 125
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 125
 Val Arg Lys Glu Val Phe Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
 50 55 60
 Thr Ala Thr Lys Lys Asp Asn Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr
 100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Glx Arg Arg Met Ser Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140

Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160

Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg
 165 170 175

Val Leu Gln Arg Cys Glu Glu Lys His Leu Ile Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Thr Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Cys Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 126

<211> 762

<212> DNA

<213> Sorghum bicolor

<400> 126

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gtgcggaagg aggtccttaa attgctgcat gcagggatta tatatcctgt gccgcacagt 60
gagtgggtga gcccagtaca agttgtgcct aaaaaaggag gcatgactgt tattataaat 120
gaaaagaacg agctaattcc gcaacgcacc gtcacaggat ggcagatgtg catagactat 180
agaaaactaa acaaagccac gagaaaggat cactttcctt taccttttat agatgagatg 240
ctagagcggg tagcaaacca ttcgttcttc tgtttcttag atggatattc agggtatcat 300
cagatcccga tccatcccga tgatcaaagc aaaaccactt ttacatgccc ttatggaact 360
tatgcttacc gtagaatgtc ttttgggtta tgtaatgcac cagcttcttt tcaaagatgc 420
atgatgtcta tattttctga tatgattgaa gagattatgg aagttttcat ggatgatttc 480
tctgtttatg gaaaagcttt tgatagttgt cttgaaaact tagacaagggt tttgcaaagt 540
tgtgaagaaa agcacttaat ccttaattgg gaaaaatgtc attttatggg tagggaagga 600
atagtgtctg gacacttagt gtctgaaagg ggtattgagg tagacaaagc tgaaattgaa 660
gtaattgaac aactacctcc acctgtgaat ataaaaggaa ttcgaagctt tcttggccat 720
gctgggtttt atcgtagatt catcaaagat ttcacgaaag tt 762
```

<210> 127

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 127

Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Gly Ile Ile Tyr Pro
1 5 10 15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20 25 30

Gly Gly Met Thr Val Ile Ile Asn Glu Lys Asn Glu Leu Ile Pro Gln
35 40 45

Arg Thr Val Thr Gly Trp Gln Met Cys Ile Asp Tyr Arg Lys Leu Asn
50 55 60

Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Ser Lys Thr
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
130 135 140

Phe Ser Asp Met Ile Glu Glu Ile Met Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Val Tyr Gly Lys Ala Phe Asp Ser Cys Leu Glu Asn Leu Asp Lys
165 170 175

Val Leu Gln Ser Cys Glu Glu Lys His Leu Ile Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser
195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Glu Ile Glu Val Ile Glu Gln
210 215 220

Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 128

<211> 762

<212> DNA

<213> Sorghum bicolor

<400> 128

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gtgcggaagg aagtcttaaa gcttttacac actaggatta tttatctcgt tcctcatagt 60
gagtgggtta gcacggtaca agttgtgcca aagaaaggag gaatgtcggg tgtaggaat 120
gagaagaacg aattcatccc tcaacaaact gtcactgggt ggcgtatgtg cattgactac 180
caaaaactca acaaggccac aaggaaagat cacttcccgt tacctttcat tgatgaaatg 240
ttgtaatggc ttacaaatca ctcgttcttt tgtttccttg aagggtattc cagatatcat 300
caaatcccga tccaccacga tgaccaaagt aagactactt tcacatgacc ctatggaact 360
tacgcatacc gacgaatgtc gttcagggtta tgtaatgctc cagcttcttt tcaacgggtgc 420
atgatgtcta ttttttccaa tatgattgag aaaatcatgg aggtattcac ggatgatttt 480
accgtatatg gcaaaacctt tgatgattgt ttagagaatt tggacaaagt cttacaattg 540
tgtgaaggaa agcacttaat cgtaaaactag gagaaatgcc attttatggg ccgagaagga 600
atagtgtctag ggcacaaggt gtccgaacgt gggatagagg tggatagagc caagattgaa 660
gttattgaaa aacttccacc tcccacaaat gtgaaagaca tccgcagttt tcttgacat 720
gcagggttct ataggcgctt catcaaagat ttcaccaagg tt 762

```

<210> 129
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 129
 Val Arg Lys Glu Val Leu Lys Leu Leu His Thr Arg Ile Ile Tyr Leu
 1 5 10 15
 Val Pro His Ser Glu Trp Val Ser Thr Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Ser Val Val Arg Asn Glu Lys Asn Glu Phe Ile Pro Gln
 35 40 45
 Gln Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
 50 55 60
 Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glx Trp Leu Thr Asn His Ser Phe Phe Cys Phe Leu Glu Gly Tyr
 85 90 95
 Ser Arg Tyr His Gln Ile Pro Ile His His Asp Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Glx Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Arg Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asn Met Ile Glu Lys Ile Met Glu Val Phe Thr Asp Asp Phe
 145 150 155 160
 Thr Val Tyr Gly Lys Thr Phe Asp Asp Cys Leu Glu Asn Leu Asp Lys
 165 170 175
 Val Leu Gln Leu Cys Glu Gly Lys His Leu Ile Val Asn Glx Glu Lys
 180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205

Glu Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Glu Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Thr Asn Val Lys Asp Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 130

<211> 761

<212> DNA

<213> Sorghum bicolor

<400> 130

gtgcgtaagg aggttttttaa gctgctgcat gcagagatta tatatcatgt gccgcacagt 60
 gagtgggtaa gccagttca agttgtgcct aaaaaggag gcatgattgt tggtacgaat 120
 gaaaagaacg agctaattcc gcaacgcacc gtcacagggt ggcggatgtg catagactat 180
 agaaaactaa acaaagccac gagaaaggat cattttcctt tacctttcat agatgagatg 240
 ctagagcgat tagcaaacca ttcgttcttc tgtttcttag atggataatt agggtatcac 300
 cagatcccaa tcaatcttga tgatcaaagc aaaaccactt ttccatgccc acatggaact 360
 tatgcttacc gtagaatgtc ttttgggtta tgtaatgcac cagcttcttt tcaaagatgc 420
 atgatgtctg tattttctaa tatgattgaa gagattatgg aattttcatg gatgatttct 480
 ctgtttatgg aaaaactttt gatagttgtc ttgaaaactt agacagggtt ttgcaaagat 540
 gtgaagaaaa gtacttagtc cttaattgga aaaaatgtca ttttatgggt agggaaggaa 600
 tagtgctggg acacctagtg tctgaaagag gtattgaggt cgacaaagct aaaattgaag 660
 taattgaaca actacctcca ctttgaata taaaaggaat tcgaagcttt cttggccatg 720
 ctgggttttta tcgtagattc attaaggact ttacaaaggt t 761

<210> 131

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 131

Val Arg Lys Glu Val Phe Lys Leu Leu His Ala Glu Ile Ile Tyr His
 1 5 10 15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30

Gly Gly Met Ile Val Val Thr Asn Glu Lys Asn Glu Leu Ile Pro Gln
 35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60

Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Glx
 85 90 95

Leu Gly Tyr His Gln Ile Pro Ile Asn Leu Asp Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Pro Cys Pro His Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Val
 130 135 140
 Phe Ser Asn Met Ile Glu Glu Ile Met Glu Ile Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Lys Thr Phe Asp Ser Cys Leu Glu Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Glu Lys Tyr Leu Val Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln
 210 215 220
 Leu Pro Pro Pro Leu Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 132
 <211> 763
 <212> DNA
 <213> Sorghum bicolor

<400> 132
 gtgcggaaag aggtcgtcaa gctctatcat gctgggatta tttatcctgt gccacatagt 60
 gagtgggtta gccctgttca agtagtgcca aagaaagaag gaatgacggt cgtaggaat 120
 gagaagaatg aactcatccc tcaacaaatt gtcactagat ggcgtatgtg tattgactat 180
 cgaaaactca acaaagctac aaagaaagat cactttccgt tacccttcat tgatgaaatg 240
 ttggaatggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac 300
 caaatcccaa tccaccaga tgaccaagaa aagactacct ttacatgcc gtattgaact 360
 tatgcatact gacgaatgtc gttcggattg tgcaatgctc tagcttcttt tccagcgggtg 420
 catgatgtct attttctcgg acatgattga gaagatcatg gaggttttca tggatgattt 480
 taccgtctat ggcaaaacct tcgatcattg tttggagaat ttagatagag tcttgacgag 540
 atgtgaggaa aatcacttaa tcttgaactg ggagaaatgt cattttatgg ttcaggaagg 600
 aatagtgtca ggacataaag tgtccgaacg tggatatagat gtggacaaag caaagattaa 660
 agttattgaa aaacttccac ctcacacgaa tgtgaaagga atccatagct ttttgggaca 720
 tgcagggttc tatagacgct tcatcaagga tttcaciaaag gtt 763

<210> 133
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 133

Val Arg Lys Glu Val Val Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro
1 5 10 15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20 25 30

Glu Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln
35 40 45

Gln Ile Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
50 55 60

Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
65 70 75 80

Leu Glu Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr
100 105 110

Thr Phe Thr Cys Pro Tyr Glx Thr Tyr Ala Tyr Glx Arg Met Ser Phe
115 120 125

Gly Leu Cys Asn Ala Leu Ala Ser Phe Gln Arg Cys Met Met Ser Ile
130 135 140

Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe
145 150 155 160

Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg
165 170 175

Val Leu Gln Arg Cys Glu Glu Asn His Leu Ile Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser
195 200 205

Glu Arg Gly Ile Asp Val Asp Lys Ala Lys Ile Lys Val Ile Glu Lys
210 215 220

Leu Pro Pro His Thr Asn Val Lys Gly Ile His Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 134

<211> 756

<212> DNA

<213> Sorghum bicolor

<400> 134

```

aaggagggttt tcaagttgct gcatgcaggg attatatatc ttgtgccgca tagtgagtgg 60
gtaagcccag ttcaagttgt gcctaaaaag ggaggcatga ctattattat gaatgaaaag 120
aacgagctaa ttccgcaacg caccgttaca gtatggcgga tgtgcataga ctatagaaaa 180
ctaaacaaaag ccacgagaga ggatcacttt cctttacctt tcatagatga gatgctagag 240
tggttagcaa accattcggt cttctgtttc ttagatggat attgagggtg tcatcagatc 300
ccgatccatc ccgatgatca aagcaaaacc acttttacat gcccatatgg aacttatgct 360
taccgtagaa tgtcttttgg gttatgtaat gcactagctt cttttcaaag atgcatgatg 420
tctatatatt ctgatatgat tgaagagatt atggaagttt tcatggatga tttctctggt 480
tatggaaaaa cttttgatag ttgtcttaaa aacttagaca aggttttgca aagatgtgaa 540
gaaaagcact tagtccttaa ttgggaaaaa tgtcatttca tggttaggga aggaatagtg 600
ctgggacact tagtgtctga aagagctatt gaggtagata aagctaaaat tgaagtaatt 660
gaacaactac gtccacctgt gaacataaaa ggaatttgaa gctttcttgg ccatgctggt 720
tttcatcgta gattcataaa agactttaca aagggtt 756

```

<210> 135

<211> 252

<212> PRT

<213> Sorghum bicolor

<400> 135

```

Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Leu Val Pro
  1             5             10             15

```

```

His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Gly Gly
      20             25             30

```

```

Met Thr Ile Ile Met Asn Glu Lys Asn Glu Leu Ile Pro Gln Arg Thr
      35             40             45

```

```

Val Thr Val Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn Lys Ala
      50             55             60

```

```

Thr Arg Glu Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met Leu Glu
      65             70             75             80

```

```

Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr Glx Gly
      85             90             95

```

```

Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Ser Lys Thr Thr Phe
      100            105            110

```

```

Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe Gly Leu
      115            120            125

```

```

Cys Asn Ala Leu Ala Ser Phe Gln Arg Cys Met Met Ser Ile Phe Ser
      130            135            140

```

```

Asp Met Ile Glu Glu Ile Met Glu Val Phe Met Asp Asp Phe Ser Val
      145            150            155            160

```

```

Tyr Gly Lys Thr Phe Asp Ser Cys Leu Lys Asn Leu Asp Lys Val Leu
      165            170            175

```

```

Gln Arg Cys Glu Glu Lys His Leu Val Leu Asn Trp Glu Lys Cys His
      180            185            190

```

Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser Glu Arg
 195 200 205

Ala Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln Leu Arg
 210 215 220

Pro Pro Val Asn Ile Lys Gly Ile Glx Ser Phe Leu Gly His Ala Gly
 225 230 235 240

Phe His Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 136
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 136
 gtgcgtaagg aggttggtcaa gcttttggag gttggggtca tatacctcat ctctgacagc 60
 gcttggtgtaa gcctagtaca ggtgggtccc aagaaatgcg gaatgacagt ggtacaaaat 120
 gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180
 tgcaagttga atgaagccac acggaaggac catttcccct tacctttcat ggatcagatg 240
 ctggagaggc ttgcagggca ggcatactac tgtttcttgg atagatattc aggatacaac 300
 caaatcgcg tagaccccag agatcaggag aagatggcct ttacatgccc ctttggcgtc 360
 tttgcttaca gaaggatgtc attcaggtta tgtaacgcac cagccacatt tcagaggtgc 420
 gtgctggcca ttttttcaga catggtggag aagagcatcg aggtatttat ggatgaattc 480
 tcgatttttg gacccttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540
 tgcgtataga ctaacttggt actaaattag gaaaaatgtc atttcatggt tcgagagggga 600
 atagtgatgg accacaatat ctcagctaga gggattgagg ttgatcaggc aaagatagac 660
 gtcattgaga agttgccacc accactgaat gttaaaggcg tcagaagttt cttagggcat 720
 gcaggtttct acaggagggtt tatcaaggac ttcaccaagg tt 762

<210> 137
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 137
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu
 1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys
 20 25 30

Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr
 35 40 45

Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn
 50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr
 85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met
 100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe
 115 120 125

Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile
 130 135 140

Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe
 145 150 155 160

Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met
 165 170 175

Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys
 180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Met Asp His Asn Ile Ser
 195 200 205

Ala Arg Gly Ile Glu Val Asp Gln Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 138

<211> 763

<212> DNA

<213> Glycine max

<400> 138

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gtgcgtaagg aggtctttaa gttcttggag gctgggctca tatatcccat ctctaatagc 60
acttaggtaa gccagttaca ggtggttccc aagaaagggtg gaatgacagt agtacagaat 120
gagaagaatg acttgatacc aacacgaact gtcactagct ggcgaaatag catcgattat 180
cgcaagctga atgaggccac ccggaaggac cacttccctc tacctttcat ggatcagatg 240
ttggagagac ttgcagggca ggcgtattat tgtttcttgg atggatactc gagatataat 300
cagattgcgg tggaccctag agaccaagag aagacgacct tcacatgccc tttttggcgt 360
ctttgcttac agaaggatgc cattcgggtt atgtaatgca ccagccacat ttcagagggtg 420
catgctggcc attttttcag acatggtgga gaaaaatatc gaggtattca tggatgactt 480
ttcagttttt gggccctcat ttgacagttg tttgaggaac ctagagatgg tacttttagg 540
gtgcgtagag actaatttag tgctgaactg ggagaagtgt cattttatgg ttcgagaggg 600
catagtcttg agccacaaga tctcagctag agggattgag gttgaccggg caaagataga 660
cgtcatagag aagctgccac caccattgaa tattaagggt gtcagaagtt tcttagggca 720
tgcaggattc tacaggagat tcataaagga ctttacaag gtt 763

```

<210> 139

<211> 254

<212> PRT

<213> Glycine max

<400> 139

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Leu Ile Tyr Pro
1 5 10 15

Ile Ser Asn Ser Thr Glx Val Ser Pro Val Gln Val Val Pro Lys Lys
20 25 30

Gly Gly Met Thr Val Val Gln Asn Glu Lys Asn Asp Leu Ile Pro Thr
35 40 45

Arg Thr Val Thr Ser Trp Arg Ile Cys Ile Asp Tyr Arg Lys Leu Asn
50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Arg Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Thr
100 105 110

Thr Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile
130 135 140

Phe Ser Asp Met Val Glu Lys Asn Ile Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Val Phe Gly Pro Ser Phe Asp Ser Cys Leu Arg Asn Leu Glu Met
165 170 175

Val Leu Glx Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Lys Ile Ser
195 200 205

Ala Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Glu Lys
210 215 220

Leu Pro Pro Pro Leu Asn Ile Lys Gly Val Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 140

<211> 762

<212> DNA

<213> Glycine max

<400> 140

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gtgcgcaagg aggttttgaa gcttctagag gttgggctta tctaccccat ctccgacagc 60
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gaaaagaatg acctgatacc aacacgaact gtcactagtt ggaaattatg catcgattac 180
cgcaagctca acgaagccac aaggaaagac catttccctc tacccttcat ggatcagatg 240
ttggagagac ttgcaggaca cgcttattat tgcttcttgg atgcatactt tggatataat 300
cagattgttg tagaccccaa ggatcaggag aagatggcct tcacatgccc ttttgggtgc 360
tttgcctata gacggattcc atttgggttg tgcaatgcac ctaccacatt ccaaattgtgc 420
atgttggcca tttttgcaga tatagtggag aaaagcatcg aagtattcat ggatgacttt 480
tcagtatttg tgccctcatt agaaagtgtg ttgaagaagt tggagatggg actacaaaga 540
tgcggtgaaa caaacttagt actaaattgg gagaagtgtc acttcatggg tcgagaaggc 600
atagtcttag gccataaaat ttcgaccoga ggaattgagg tagaccaaac aaagattgat 660
gtcattgaaa agttgccacc accatcaaat gttaaaggca tcaggagctt cctaggacaa 720
gccaggttct acagaagatt catcaaggac ttcacaaaag tt 762

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<210> 141
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 141
 Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Pro Val Leu Val Val Ser Lys Lys
 20 25 30
 Glu Gly Met Thr Val Ile Arg Asn Glu Lys Asn Asp Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Ser Trp Lys Leu Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly His Ala Tyr Tyr Cys Phe Leu Asp Ala Tyr
 85 90 95
 Phe Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Met
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Ile Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Met Cys Met Leu Ala Ile
 130 135 140
 Phe Ala Asp Ile Val Glu Lys Ser Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Val Pro Ser Leu Glu Ser Cys Leu Lys Lys Leu Glu Met
 165 170 175
 Val Leu Gln Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205

Thr Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Ser Asn Val Lys Gly Ile Arg Ser Phe Leu Gly Gln
 225 230 235 240

Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 142
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 142
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 tcataggtta gtcctgttca tggtgctctg aaaaagggag gtatgacagt gataaagaat 120
 gatagagatg agttaattcc tacaagaata gttactggat ggaggatggg tattgattac 180
 aagaagctaa atgaagccac caggaaagac cattaccgc ttcccttcat ggatcaaagt 240
 cttgagagac ttgcagggca atcttcctac tatttattag atggatactc gggctacaat 300
 caaattgcag tggatcctca ggaccaagaa aagacagctt tcacatgtcc ttttggtgta 360
 tttgcttata gccgcatgtc gttcggttta tgtaatgccc caactacttt ccagagatgt 420
 atgatggcaa ttttgctga catggtaaag aaatgtattg aagtttttat ggacgatttc 480
 tctgtctttg gtgcatcttt tgaaaattgc ctacgaaatt tagagaaagt gttacaacgc 540
 tatgaagaat ctaatttggg gctcaactgg gaaaaatgtc actttatggg tcaagaaggt 600
 atcatgctgg gacacaagat ttctagaaga ggaattaagg tggataaggc aaagattgag 660
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 gctagattct atcgatgatt tatcaaggac ttcaccaaag tt 762

<210> 143
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 143
 Val Arg Lys Glu Val Ile Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu
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 20 25 30
 Gly Gly Met Thr Val Ile Lys Asn Asp Arg Asp Glu Leu Ile Pro Thr
 35 40 45
 Arg Ile Val Thr Gly Trp Arg Met Gly Ile Asp Tyr Lys Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Gln Ser Ser Tyr Tyr Leu Leu Asp Gly Tyr
 85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr
 100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe
 115 120 125

Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140

Phe Ala Asp Met Val Lys Lys Cys Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160

Ser Val Phe Gly Ala Ser Phe Glu Asn Cys Leu Ala Asn Leu Glu Lys
 165 170 175

Val Leu Gln Arg Tyr Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser
 195 200 205

Arg Arg Gly Ile Lys Val Asp Lys Ala Lys Ile Glu Val Ile Asp Lys
 210 215 220

Leu Pro Pro Leu Val Asn Val Arg Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Arg Phe Tyr Arg Glx Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 144

<211> 761

<212> DNA

<213> Glycine max

<400> 144

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 gataaagatg agttgatatc cacaaggacc gtcaccgggt ggagaatgtg cattgactat 180
 cgaaagctga atgatgcacc cggaaggacc attatccact ccctttcatg ggccatatgc 240
 ttgaaagact tgttgggcaa tcctattatt gttttctaga tggatattat gggtataatc 300
 agattgttgt agatcccaaa gatcaagaga agacagcttt cacctaccct tttggtgtat 360
 tcgcatatca gtgcatgcct tttggtctat gcaatgcccc agctacattt cagaggtgta 420
 tgatggctat tttttctgat atggtggaaa tatgcattga agttttcatg gacgatttct 480
 ctatttttgg gccatccttt gaagggtgct tatcaaactt tgaaaaagta ttaaagagat 540
 gtgaagagtc caatctagtt ctcaattgga agaaatgccca tttcatgggt caagaaggaa 600
 taatgttggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
 taattgagaa actacttgct cccatgaatg tcaagggaat aagaagcttc ttaggacatg 720
 cagggttcta caggcgattc ataaaagact tcaccaaagt t 761

<210> 145

<211> 254

<212> PRT

<213> Glycine max

<400> 145

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Pro Met Gln Val Val Pro Lys Lys
20 25 30

Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Gly His Met
65 70 75 80

Leu Glu Arg Leu Val Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
85 90 95

Tyr Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
100 105 110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Gln Cys Met Pro Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
130 135 140

Phe Ser Asp Met Val Glu Ile Cys Ile Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Lys
165 170 175

Val Leu Lys Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Lys Lys
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210 215 220

Leu Leu Ala Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 146

<211> 762

<212> DNA

<213> Glycine max

<400> 146

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gataagaatg atcttattcc tacacagaca atcattaggt ggcaaagtgt tattgactat 180
cacaagttga atgatgtcac caagaaggac cattttcctc tgccattcat ggaccaaagt 240
ttagagaggt tagctggcca agctttttat tgttttttgg atggttattc tgggtataac 300
caaatagcgg tgcatcttaa agatcaagag aagactacta tcatatgccc atttggtgtc 360
tttgcttaca gacaaatgtc atttgaactg tgtaatgccc ctaccacctt ctagagattc 420
atgatggcca tttttgctga ccttgtggag aaatgcatag aggtgttcat gaatgatttc 480
tctattttcg gctcttcctt ttatcattgt ttatccaacc tggaattagt gttacaacgg 540
tgtgCGgaaa ccaatttgtt gatgaactgg gagaaatgtc atttcatggt ccaagagggg 600
attgtcttag gccacaagat ctcttccaga gggttggaag tggacaaggc aaaaattgat 660
gttattgaga agttgcctcc acctatgaat gtgaaaggca tccgaagttt tctcgaatat 720
gttggaattt ataggaggtt catcaaagac ttcacgaaag tt 762

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<210> 147
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 147
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Ser Asn Glx Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile His Asn Asp Lys Asn Asp Leu Ile Pro Thr
 35 40 45
 Gln Thr Ile Ile Arg Trp Gln Met Cys Ile Asp Tyr His Lys Leu Asn
 50 55 60
 Asp Val Thr Lys Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Gln Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val His Leu Lys Asp Gln Glu Lys Thr
 100 105 110
 Thr Ile Ile Cys Pro Phe Gly Val Phe Ala Tyr Arg Gln Met Ser Phe
 115 120 125
 Glu Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Phe Met Met Ala Ile
 130 135 140
 Phe Ala Asp Leu Val Glu Lys Cys Ile Glu Val Phe Met Asn Asp Phe
 145 150 155 160
 Ser Ile Phe Gly Ser Ser Phe Tyr His Cys Leu Ser Asn Leu Glu Leu
 165 170 175
 Val Leu Gln Arg Cys Ala Glu Thr Asn Leu Leu Met Asn Trp Glu Lys
 180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205

Ser Arg Gly Leu Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Glu Tyr
 225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 148
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 148
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 gcttggttaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaat 120
 gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180
 tgcaagttga atgaagccac acggaaggac catttcccct tacctttcat ggatcagatg 240
 ctggagaggc ttgcagggca ggcatactac tgtttcttgg atagatattc aggatacaac 300
 caaatcgcg tagaccccag agatcaggag aagatggcct ttacatgccc ctttggcgctc 360
 tttgcttaca gaaggatgtc attcaggtta tgtaacgcac cagccacatt tcagaggtgc 420
 atgctggcca ttttttcaga catgggtggag aagagcatcg aggtatttat ggatgaattc 480
 tcgatttttg gacccttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540
 tgcgtataga ctaacttggg actaaattag gaaaaatgtc atttcatggt tcgagagggg 600
 atagtgatgg gccacaatat ctcagctaga gggattgagg ttgatcagac aaagatagac 660
 gtcattgaga agttgccacc accactgaat gttaaaggcg tcagaagttt cttagggcat 720
 gcaggtttct acaggaggtt cataaaagac ttcacaaagg tt 762

<210> 149
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 149
 Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu
 1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys
 20 25 30

Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr
 35 40 45

Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn
 50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr
 85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met
 100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe
 115 120 125

Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile
 130 135 140

Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe
 145 150 155 160

Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met
 165 170 175

Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys
 180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Met Gly His Asn Ile Ser
 195 200 205

Ala Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 150
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 150
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 gcatgggtta gccctgtgca ggttgtcccc aagaaagaag gtaagacagt cattaaggat 120
 gaaaaggatg agttgatatc cacaaggact atcaccgggt ggagaatgtg cattgactat 180
 cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaagt 240
 cttgaaagac ttgccgggca atcttattat tgttttctgg atggatattc tggttataat 300
 cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctaccc ttttggtgta 360
 ttcgcctatc ggcgcatgcc ctttggtttg tgcaatgcc cagctacatt tcagaggtgt 420
 atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatttc 480
 tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540
 cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600
 atagtgtggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
 taatagagaa actacctcct cccatgaatg tcaagggaat aagaagcttc ctaggacatg 720
 cagggttcta caagcgattc atcaaagatt tcacaaaggt t 761

<210> 151
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 151

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20 25 30

Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
35 40 45

Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
100 105 110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
130 135 140

Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Phe
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
165 170 175

Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210 215 220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 152

<211> 762

<212> DNA

<213> Glycine max

<400> 152

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gatagaaatg agctaattcc tacaagaaga gtcaccagat ggagaatgtg tattgattat 180
aggaagctca atgaagccac aagaaaagac cattaccacac ttcccttcat ggatcaaag 240
cttaagagac ttgcaaggca atccttctac cgtttcttgg acggatactc aggttacaat 300
cagattgcag tggatcctca ggatcaagaa aaaacagctt ttacatgtcc tttcagtgtt 360
tttgcttatt gccgcatgcc gttcgggtta tgtaatgcct ctactacttt tcagagatgt 420
atgatggcaa tttttgatga catggtagag aaatgtattg aagtctttat ggatgatttt 480
tcgttctttg gtgcatcttt tggaaattgc ttagcaaatt tagagaaagt gttacaacgt 540
tgtgaaaaat ctaatttggg gcttaactgg gaaaaatgtc actttatggg acaagaaggt 600
attgtgctag gacacaaaat ctctaaaaga ggaattgagg tggttaaaga aaaactagat 660
gttattgata aacttcacc cccagttaat gtaaaaggca tacacagttt tttgggtcat 720
gttgatttt atcgcgcat cataaaggac ttcaccaaag tt 762

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<210> 153
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 153
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 Ile Ser Asp Ser Ser Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Lys Asn Asp Arg Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Arg Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Lys Arg Leu Ala Arg Gln Ser Phe Tyr Arg Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Phe Ser Val Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Ser Thr Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Asp Asp Met Val Glu Lys Cys Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Phe Phe Gly Ala Ser Phe Gly Asn Cys Leu Ala Asn Leu Glu Lys
 165 170 175
 Val Leu Gln Arg Cys Glu Lys Ser Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205

Lys Arg Gly Ile Glu Val Val Lys Glu Lys Leu Asp Val Ile Asp Lys
 210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile His Ser Phe Leu Gly His
 225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 154
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 154
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 gataaagatg agttgatatc cacaaggact gtcaccgggt gagaatgtgc attgactatc 180
 ggaagctgaa tgatgccacc cagaaggacc attattcact ccctttcatg gaccagatgc 240
 ttgaaagact tgccggacaa tcctattatt gttttctgaa tggatactct ggctataatc 300
 agattgtggt agatcccaaa gatcaggaga aaactgcttt cacctgcctt tttggtgtat 360
 ttgcatacaa gcgtatgcat tttggcttgt gtaatgctcc aactacgtgt cagagggtga 420
 tgatgactat tttttctggt atcgtggaaa aatgcattga acttttcatg gacgatttct 480
 ctattttttg gccatctttt gaaggctact tatcaaacct tgaaagagta ttacagagat 540
 gtgaagagtc taatctagtt ctcaattggg agaaatgcca tttcatgggt caagaaggaa 600
 tagtgctggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
 taattgagaa actacctcct cccatgattg tcaagggaat aagaagcctc ctaggacatg 720
 tagggttcta caggcgattc atcaaagact tcacaaagggt t 761

<210> 155
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 155
 Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Asp Leu Ile Tyr Pro
 1 5 10 15

Ile Ser Asp Ser Thr Trp Val Ser Pro Val Gln Val Val Pro Glu Lys
 20 25 30

Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
 35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60

Asp Ala Thr Gln Lys Asp His Tyr Ser Leu Pro Phe Met Asp Gln Met
 65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asn Gly Tyr
 85 90 95

Ser Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
100 105 110

Ala Phe Thr Cys Leu Phe Gly Val Phe Ala Tyr Lys Arg Met His Phe
115 120 125

Gly Leu Cys Asn Ala Pro Thr Thr Cys Gln Arg Cys Met Met Thr Ile
130 135 140

Phe Ser Gly Ile Val Glu Lys Cys Ile Glu Leu Phe Met Asp Asp Phe
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Tyr Leu Ser Asn Leu Glu Arg
165 170 175

Val Leu Gln Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210 215 220

Leu Pro Pro Pro Met Ile Val Lys Gly Ile Arg Ser Leu Leu Gly His
225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 156

<211> 762

<212> DNA

<213> Glycine max

<400> 156

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gaaaaagatg agttgataac cacaaggact atcaccgggt ggagaatgtg cattgactat 180
cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaagt 240
cttgaaagac ttgccgggca atcttattat tgttttcttg atggatattc tggttataat 300
cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctaccc ttttggtgta 360
ttcgctatc ggcgcatgcc ctttggtttg tgcaatgccc cagctacatt tcagaggtgt 420
atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatgtc 480
tctatttttg ggccatcttt tgaagggtgc ttatcaaata ttgaaagagt attaaagaga 540
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600
atagtgttgg ggcataaaat ttcagtaaga gggatagagg tggacaaggc aaagattgat 660
gtaatagaga aactacctcc tcccatgaat gtcaagggaa taagaagctt cctaggacat 720
gcagggttct acaagcgatt catcaaagac ttctcaaaag tt 762
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<210> 157

<211> 254

<212> PRT

<213> Glycine max

<400> 157

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20 25 30

Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
35 40 45

Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
100 105 110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
130 135 140

Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Val
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
165 170 175

Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210 215 220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Ser Lys Val
245 250

<210> 158

<211> 761

<212> DNA

<213> Glycine max

<400> 158

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gtgcggaagg aggttcttaa gctcctggaa gcagggtca tctatcttat ctcagatagt 60
gttgggtgag tccagtgcac gtggttccca agaaggggtg gaagactgtg gtgagaaatg 120
agaaaaatga cctcattcta acccgaactg tcacaggatg gagaatgtgc atagattatc 180
ggaagtggaa tgatgccatc aagaaggatc acttccctct accattcata gatcagatgc 240
ttgagagggt agcaagccag tctttctatt atttcttggg tgaatattct agatacaatc 300
agattgctat acatcccaag gaccaagaga agattgcatt tacatgcccc tttgggtgtc 360
ttgcctatag aaggatgcca ttgaactat gcaatgctcc agctaccttt tagaggcata 420
tgctagccat attcgctaac atggtggaga aatgcatcga agtggttcata gatgattttt 480
cgggtgttgg tccatccttt gtttgttgtt tgaccaattt agagctagtg ttgaagtact 540
gtgaggagac aaatttagta ttgaattggg agaaatgtca tttcatgggc caagaaggaa 600
ttatgttggg gcataaaatt tttgctagag gtattgaggt ggacaaggcc aaaattgatg 660
ttattgaaaa gctgcctcca ccagtcaatg taaaaggcat caggagtttt cttggacaca 720
ctggtttctt caggcgtttc atcaaggact tcacaaaagt t 761

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<210> 159

<211> 254

<212> PRT

<213> Glycine max

<400> 159

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Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu
  1              5              10              15

```

```

Ile Ser Asp Ser Ala Trp Val Ser Pro Val His Val Val Pro Lys Lys
      20              25              30

```

```

Gly Gly Lys Thr Val Val Arg Asn Glu Lys Asn Asp Leu Ile Leu Thr
      35              40              45

```

```

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
      50              55              60

```

```

Asp Ala Ile Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
      65              70              75              80

```

```

Leu Glu Arg Leu Ala Ser Gln Ser Phe Tyr Tyr Phe Leu Asp Glu Tyr
      85              90              95

```

```

Ser Arg Tyr Asn Gln Ile Ala Ile His Pro Lys Asp Gln Glu Lys Ile
      100             105             110

```

```

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
      115             120             125

```

```

Glu Leu Cys Asn Ala Pro Ala Thr Phe Glx Arg His Met Leu Ala Ile
      130             135             140

```

```

Phe Ala Asn Met Val Glu Lys Cys Ile Glu Val Phe Ile Asp Asp Phe
      145             150             155             160

```

```

Ser Val Phe Gly Pro Ser Phe Val Cys Cys Leu Thr Asn Leu Glu Leu
      165             170             175

```

```

Val Leu Lys Tyr Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
      180             185             190

```

Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Phe
 195 200 205

Ala Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Thr Gly Phe Phe Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 160
 <211> 762
 <212> DNA
 <213> Pisum sativum

<400> 160
 gtgcgcaagg aagtactcaa gttgtagat tccgggaatga ttaccccat ttctgacagc 60
 tcgtgggtaa gtccagtgc cgtggtacca aagaaaggag gaacctcagt aattttaaat 120
 gaaaagaatg aactgatccc aactcgaca gtgacagggt ggcgagtatg catcgatcac 180
 agaagactga acacagcaac aagaaaggat cattttcctc tcccttttat tgatcaaagt 240
 ttagaaagac ttgcagggtca tgagtattat tgctttctgg atggatattc gggatacaat 300
 caaattgttg tagccccgga agatcaggaa aaaactgcat ttacatgtcc ttatggtatt 360
 ttcgcttaca gacggatgcc atttgggcta tgcaatgccc cagctacttt tcagagggtg 420
 atgacatcta tattctccga catgcttgaa aagtatatga aggtgtttat ggatgatttc 480
 tctgtgtttg gttcttcttt tgataattgt ttagctaact tgtctctgt tttgcaaaga 540
 tgtcaggaaa ctaaccttgt tctcaattgg gagaaatgtc atttcatggt gcaggaaagg 600
 attgtgctag gacacaaaat ttcccacaaa ggaattgaag tggacaaagc caaagtggag 660
 gttatagcta acctccacc tccggtgaat gaaaaaggga taaggagttt tttgggtcat 720
 gcagggtttt atcgcagggt catcaaagac ttcacaaagg tt 762

<210> 161
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 161
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ser Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20 25 30
 Gly Gly Thr Ser Val Ile Leu Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Val Cys Ile Asp His Arg Arg Leu Asn
 50 55 60
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95

Ser Gly Tyr Asn Gln Ile Val Val Ala Pro Glu Asp Gln Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Tyr Gly Ile Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Thr Ser Ile
 130 135 140
 Phe Ser Asp Met Leu Glu Lys Tyr Met Lys Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Ser Ser Phe Asp Asn Cys Leu Ala Asn Leu Ser Leu
 165 170 175
 Val Leu Gln Arg Cys Gln Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 His Lys Gly Ile Glu Val Asp Lys Ala Lys Val Glu Val Ile Ala Asn
 210 215 220
 Leu Pro Pro Pro Val Asn Glu Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 162
 <211> 762
 <212> DNA
 <213> Pisum sativum

<400> 162
 gtgcgtaagg aggtctttaa actattggat gcgggaatga tttacccgat ctcgatagat 60
 ccgtgggtta gtcccggtgca cgtgggttccg aagaaggggtg gaatgaccgt aatccgtaat 120
 gacaaagacg aattgatccc gactaaagtt gcaacggggt ggagaatatg tatagattat 180
 agacagttga ataccgcgac tcgaaaggac catittccac tcccatttat ggatcaaatg 240
 cttgaaagac tatcgggccca acaatactat tgtttcttgg acggctactc cgggtacaac 300
 caaattgcgg ttgacccggt tgatcatgag aagacggcct tcacgtgtcc gtttggagtg 360
 ttcgcataca gaaaaatgcc ctttgggctg tgcaatgcac cggcgacttt ccaacgatgc 420
 gtcctagcca tttttgccga tctaataagag aaaacaatgg acgtcttcat ggatgacttc 480
 tcggtatttg gtgggacggt tagtctatgc ttggcaaat tgaagacggt gttggaaagg 540
 tgtgtgaaga ccaatttggt gctaaattgg gaaaagtgtc acttcatggt gaccgagggg 600
 atcgtgctag gccacaaaagt ctctaaaagg gggcttgaag tgatagagc taaggttgaa 660
 gtaattgaaa aattaccccc tccggtgaat gtgaaaggca tccgtagctt tttggggcac 720
 gcggggtttt accggcgctt cattaaagac ttctcaaaag tt 762

<210> 163
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 163

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
1 5 10 15

Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
20 25 30

Gly Gly Met Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
35 40 45

Lys Val Ala Thr Gly Trp Arg Ile Cys Ile Asp Tyr Arg Gln Leu Asn
50 55 60

Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
65 70 75 80

Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Val Asp His Glu Lys Thr
100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile
130 135 140

Phe Ala Asp Leu Ile Glu Lys Thr Met Asp Val Phe Met Asp Asp Phe
145 150 155 160

Ser Val Phe Gly Gly Thr Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
165 170 175

Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190

Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
195 200 205

Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
245 250

<210> 164

<211> 762

<212> DNA

<213> Pisum sativum

<400> 164

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gtgcggaagg aggtctttaa attgttggat gcgggggatga tttacccgat ctcggatagt 60
ccatgggtta gtcctgtgca cgttgttccg aagaaggggg ggattaccgt aatccggaat 120
gacaaggatg aattgatccc cactaaagtt gaaacggggg ggagaatgtg tattgattat 180
aggcgggttg ataccgcgac tcgaaaagac cattttccac tcccatttat ggatcaaatg 240
ctcgaaagac tatcggggcca acaatattat tgttttttgg acggctactc cgggtacaac 300
caaattgcgg ttgaccgggc cgatcatgag aagacgggctt tcacatgtcc gtttggagtg 360
ttcgcatacc gaaaaatgcc ctttgggctg tgcaatgcac cggcgacctt ccaacgatgt 420
gtccaagcca tttttgtcga tctgatatag aaaacaatgg aagtcttcat ggatgacttc 480
tcggtatatt gtgggtcttt tagtctatgc ttggcgaaact tgaaaacggg gttggagaga 540
tgtgtgaaga ccaatttggg gcttaattgg gagaagtgtc acttcatggg gaccgagggg 600
atcgtgctag gccacaaagt ctctagaagg gggcttgaag tggatagagc taaggttgaa 660
gtgatagaaa aattacctcc tccggtgaat gtgaagggca tccgaagctt tttggggcac 720
gccgggttct accggcgctt cattaaagat ttcacaaagg tt 762

```

<210> 165

<211> 254

<212> PRT

<213> Pisum sativum

<400> 165

```

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
  1              5              10              15

```

```

Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
      20              25              30

```

```

Gly Gly Ile Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
      35              40              45

```

```

Lys Val Glu Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Arg Leu Asn
      50              55              60

```

```

Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
      65              70              75              80

```

```

Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
      85              90              95

```

```

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Ala Asp His Glu Lys Thr
      100             105             110

```

```

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
      115             120             125

```

```

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Gln Ala Ile
      130             135             140

```

```

Phe Val Asp Leu Ile Glu Lys Thr Met Glu Val Phe Met Asp Asp Phe
      145             150             155             160

```

```

Ser Val Phe Gly Gly Ser Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
      165             170             175

```

```

Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
      180             185             190

```

Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
195 200 205

Arg Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated

<221> misc_feature
<222> 6, 15, 16, 18
<223> n = A,T,C or G

<400> 166
gtgcgnaarg argtnntnaa ryt

23

<210> 167
<211> 8
<212> PRT
<213> Consensus sequence

<400> 167
Val Arg Lys Glu Val Leu Lys Leu
1 5

<210> 168
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated

<221> misc_feature
<222> 7
<223> n = A,T,C or G

<400> 168
aacyttngwr aartcytttda traa

24

<210> 169
<211> 8
<212> PRT
<213> Consensus sequence

<400> 169

B4
center

Val Lys Ser Phe Asp Lys Ile Phe
1 5